



CCACGGTCCGGTCAGCTCTGGTTCGGAGAACGAGCGGCTGGCGTGGGCCATCCGGGGAAATGGGC
GCCCTCGTAGCCTAGTGTGGGGGCAAAAGGGTCTTGCCGGCCTCGCTCGTGAGGGCGTAT
CTGGCGCCTGAGCGGGCGTGGGAGCCCTTGGAGCCCGCAGCAGGGGCGACACCCGGAAACCG
GCCTAGCGCCCGGACCATGAACGGGAGGCCATCTGCGAGGCCCTGCCACCATTCCTACCA
CAAACTCGCCGACCTGCGCTACCTGAGCCGGGGCCCTCTGGCACTGTGTCGTCGCCGCCACG
CAGACTGGCGCTCCAGGTGGCCGTGAAGCACTGACATCCACACTCCGCTGCTCGACAGTGAA
AGAAAGGATGCTTAAAGAGAGAGCTGAATTTTACACAAAGCTAGATTAGTTACATTCTTCCAAAT
TTTGGGAAATTTGCAATGAGCCTGAATTTTGGGAATAGTTACTGAATACATGCCAAATGGATCAT
TAAATGAACTCTACATAGGAAACTGAATATCCTGATGTTGCTTGCCCATTGAGATTTTCGCATC
CTGCATGAAATTTGCCCTTGGTGTAAATTAACCTGCACAAATAGACTCCTCCTTACTTCATCATGA
CTTGAAGACTCAGAAATATCTTATTTGGCAATGAATTTTCACTGTTAAGATTGCAGATTTTGGTTTAT
CAAAAGTGGCGCATGATGTCCTCTCACAGTACGAGTAGCAAACTCTGCACCCAGAGGAGGACA
ATTATCTATATGCCACCTGAAACTATGAACCTGGACAAAATCAAGGCCAGTATCAAGCACGA
TATATAGCTATGCAGTTATCACATGGGAAGTGTATCCAGAAAACAGCCCTTTTGAAGATGTCA
CCAACTCTTGCAGATAATGTATAGTGTGTCAAGGACATCGACCTGTTATTAATGAAGAAAGT
TTGCCATATGATATACCTCACCGAGCACGTATGATCTCTCTAATAGAAAGTGTGATGGGCACAAA
TCCAGATGAAGAGACCATCTTTCTTAAATGTTTAAATAGAACTTGAACCCAGTTTGTAGAAACATTTG
AAGAGATAACTTTTCTTGAAGCTGTTATTCAGCTAAAGAAAACAAAGTTACAGAGTGTTCAGAGT
GCCATTACCTATGTGACAAAGAGAAAATGGAAATTAATCTGTGAACATACCTGTAAATCATGTGTC
ACAAGAGGAATCATGTGGATCCTCTCAGCTCCAATGAATAATAGTGGTTCTCCTGAAACTTCAAGGT
CCCTGCCAGCTCCTGAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAG
CTGCATCACTGTCTGGAAATCAAGTTGGATAGCACCAATTTCTGGATCTCAAGGGCTGCATT
CTGTGATCAAGACCATTCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACT
CAGAACGTCTGGAGCCTGGTATAGCCAGGAGTGGATCCAGAGCAAAAGGAGACATTTGTGAAC
CAAAATGACAGAGCCTGCCCTTAAACCGTCCAGTGTAGATGCCCTTCTGTCCAGGACTTGATCATGAA
AGAGGACTATGAACCTTGTAGTCCAAAGCTTACAAAGGACCTCAAAAGTCAAGACATTAAGTACACA
CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAA
ATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCA
AAATAAAGCATGTAAGTGACTGTTTTCAGAGAAATGTGTTTTCATAAAGGATATTTATAAA
AAAAAAA

(SEQ ID NO: 1)

FIG. 1

FIG. 2

(SEQ ID NO: 2)

TTTTTATGGG AATCGCAGCT TGGAAGAGAC AGARCAATTC CAGAAWTAAA TTGRAATTGA
AGATTTAACC AATGTTGTTT TAAAATATTC TAACTTCAAA GAATGATGCC AGAACTTWAA
AAGGGRCTGC GCAGAGTAGC AGGGGCCCTG GAGGGCGCGG CCTGAATCCT GATTGCCCTT
CTGCTGAGAG GACACACGCA GCTGAAGATG AATTTGGGAA AAGTAGCCGC TTGCTACTTT
AACTATGGAA GAGCAGGGCC ACAGTGAGAT GGAAATAATC CCATCAGAGT CTCACCCCCA
CATTCAATTA CTGAAAAGCA ATCGGGAAC TCTGGTCACT CACATCCGCA ATACTCAGTG
TCTGGTGGAC AACTTGCTGA AGAATGACTA CTTCTCGGCC GAAGATGCGG AGATTGTGTG
TGCCTGCCCC ACCCAGCCTG ACAAGGTCCG CAAAATTCTG GACCTGGTAC AGAGCAAGGG
CGAGGAGGTG TCCGAGTTCT TCCTCTACTT GCTCCAGCAA CTCGCAGATG CCTACGTGGA
CCTCAGGCCT TGGCTGCTGG AGATCGGCTT CTCCCCTTCC CTGCTCACTC AGAGCAAAGT
CGTGGTCAAC ACTGACCCAG TGAGCAGGTA TACCCAGCAG CTGCGACACC ATCTGGGCCG
TGACTCCAAG TTCGTGCTGT GCTATGCCCA GAAGGAGGAG CTGCTGCTGG AGGAGATCTA
CATGGACACC ATCATGGAGC TGGTTGGCTT CAGCAATGAG AGCCTGGGCA GCCTGAACAG
CCTGGCCTGC CTCCTGGACC ACACCACCGG CATCCTCAAT GAGCAGGGTG AGACCATCTT
CATCCTGGGT GATGCTGGGG TGGGCAAGTC CATGCTGCTA CAGCGGCTGC AGAGCCTCTG
GGCCACGGGC CGGCTAGACG CAGGGGTCAA ATTCTTCTTC CACTTTCGCT GCCGCATGTT
CAGCTGCTTC AAGGAAAGTG ACAGGCTGTG TCTGCAGGAC CTGCTCTTCA AGCACTACTG
CTACCCAGAG CGGGACCCCG AGGAGGTGTT TGCCTTCCTG CTGCGCTTCC CCCACGTGGC
CCTCTTCACC TTCGATGGCC TGGACGAGCT GCACTCGGAC TTGGACCTGA GCCGCGTGCC
TGACAGCTCC TGCCCCTGGG AGCCTGCCCA CCCCCTGGTC TTGCTGGCCA ACCTGCTCAG
TGGAAGCTG CTCAAGGGGG CTAGCAAGCT GCTCACAGCC CGCACAGGCA TCGAGGTCCC
GCGCCAGTTC CTGCGGAAGA AGGTGCTTCT CCGGGGCTTC TCCCCAGCC ACCTGCGCGC
CTATGCCAGG AGGATGTTCC CCGAGCGGGC CCTGCAGGAC CGCCTGCTGA GCCAGCTGGA
GGCCAACCCC AACCTCTGCA GCCTGTGCTC TGTGCCCCCTC TTCTGCTGGA TCATCTTCCG
GTGCTTCCAG CACTTCCGTG CTGCCTTTGA AGGCTCACCA CAGCTGCCCC ACTGCACGAT
GACCCTGACA GATGTCTTCC TCCTGGTCAC TGAGGTCCAT CTGAACAGGA TGCAGCCCAG
CAGCCTGGTG CAGCGGAACA CACGCAGCCC AGTGGAGACC CTCCACGCCG GCCGGGACAC
TCTGTGCTCG CTGGGGCAGG TGGCCCACCG GGGCATGGAG AAGAGCCTCT TTGTCTTCAC
CCAGGAGGAG GTGCAGGCCT CCGGGCTGCA GGAGAGAGAC ATGCAGCTGG GCTTCCTGCG
GGCTTTGCCG GAGCTGGGCC CCGGGGGTGA CCAGCAGTCC TATGAGTTTT TCCACCTCAC
CCTCCAGGCC TTCTTTACAG CCTTCTTCCT CGTGCTGGAC GACAGGGTGG GCACTCAGGA
GCTGCTCAGG TTCTTCCAGG AGTGGATGCC CCCTGCGGGG GCAGCGACCA CGTCTGCTA

FIG. 3A

TCCTCCCTTC CTCCCGTTCC AGTGCCTGCA GGGCAGTGGT CCGGCGCGGG AAGACCTCTT
CAAGAACAAG GATCACTTCC AGTTCACCAA CCTCTTCCTG TCGGGGCTGT TGTCCAAAGC
CAAACAGAAA CTCCTGCGGC ATCTGGTGCC CGCGGCAGCC CTGAGGAGAA AGCGCAAGGC
CCTGTGGGCA CACCTGTTTT CCAGCCTGCG GGGCTACCTG AAGAGCCTGC CCCGCGTTCA
GGTCGAAAGC TTCAACCAGG TGCAGGCCAT GCCCACGTTC ATCTGGATGC TCGCTGCAT
CTACGAGACA CAGAGCCAGA AGGTGGGGCA GCTGGCGGCC AGGGGCATCT GCGCCAACTA
CCTCAAGCTG ACCTACTGCA ACGCCTGCTC GGCCGACTGC AGCGCCCTCT CCTTCGTCCT
GCATCACTTC CCCAAGCGGC TGGCCCTAGA CCTAGACAAC AACAATCTCA ACGACTACGG
CGTGCGGGAG CTGCAGCCCT GCTTCAGCCG CCTCACTGTT CTCAGACTCA GCGTAAACCA
GATCACTGAC GGTGGGGTAA AGGTGCTAAG CGAAGAGCTG ACCAAATACA AAATTGTGAC
CTATTTGGGT TTATACAACA ACCAGATCAC CGATGTCGGA GCCAGGTACG TCACCAAAT
CCTGGATGAA TGCAAAGGCC TCACGCATCT TAAACTGGGA AAAAACAAAA TAACAAGTGA
AGGAGGGAAG TATCTCGCCC TGGCTGTGAA GAACAGCAAA TCAATCTCTG AGGTTGGGAT
GTGGGGCAAT CAAGTTGGGG ATGAAGGAGC AAAAGCCTTC GCAGAGGCTC TCGGGAACCA
CCCCAGCTTG ACCACCCTGA GTCTTGCGTC CAACGGCATC TCCACAGAAG GAGGAAAGAG
CCTTGCGAGG GCCCTGCAGC AGAACACGTC TCTAGAAATA CTGTGGCTGA CCCAAAATGA
ACTCAACGAT GAAGTGGCAG AGAGTTTGGC AGAAATGTTG AAAGTCAACC AGACGTAAAA
GCATTTATGG CTTATCCAGA ATCAGATCAC AGCTAAGGGG ACTGCCCAGC TGGCAGATGC
GTTACAGAGC AACACTGGCA TAACAGAGAT TTGCCTAAAT GGAAACCTGA TAAAACCAGA
GGAGGCCAAA GTCTATGAAG ATGAGAAGCG GATTATCTGT TTCTGAGAGG ATGCTTTCCT
GTTTCATGGGG TTTTGGCCCT GGAGCCTCAG CAGCAAATGC CACTCTGGGC AGTCTTTTGT
GTCAGTGTCT TAAAGGGGCC TCGCAGGCG GGACTATCAG GAGTCCACTG CCTYCATGAT
GCAAGCCAGC TTCCTGTGCA GAAGGTCTGG TCGGCAAACT CCCTAAGTAC CCGCTACAAT
TCTGCAGAAA AAGAATGTGT CTTGCGAGCT GTTGTAGTTA CAGTAAATAC ACTGTGAAGA
GAAAAA AAAA ACGGACGCGT GG (SEQ ID NO: 7)

FIG. 3B

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCACPTQP
DKVRKILDVLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLLEIGFSPSLLTQSKVVVNTDPVSRYT
QQLRHHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESGLNSLACLDDHTTGILNEQG
ETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFHFHRCRMFSCFKESDRCLCLQDLLFKHYCY
PERDPEEVFAFLLRFPHVALFTFDGLDELHSDLDLSRVPDSSCPWEPAHPLVLLANLLSGKLLKG
ASKLLTARTGIEVPRQFLRKKVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSV
PLFCWIIIFRCFQHFRAAFEGSPQLPDCMTMTLTDVFLLVTEVHLNRMQPSLLVQRNTRSPVETLHA
GRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELPGGDQSQSYEFFHLTL
QAFFTAFFLVLDLDRVGTQELLRRFFQEWMPAGAAATTSCTCYPPFLPFQCLQSGGPAREDLFKNKDH
QFTNLFCLGLLSKAKQKLLRHLVPAAALRRKRKALWAHLFSSLRGYLKS LPRVQVESFNQVQAMP
TFIWMRLRCIYETQSKVQGLAARGICANYLKLTYCNACSDCSALSFVLHHFPKRLALDLDDNNNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSSEELTKYKIVTYLGLYNNQITDVGARYVTKIL
DECKGLTHLKLGNKIITSEGGKYLALAVKNSKSI SEVGMWGNQVGDEGAKAFEAALRNHPSLTTL
SLASNGISTEGGKSLARALQQNTSLEILWLTONELNDEVAESLAEMLKVNQTLKHLWLIONQITA
KGTAQLADALQSNLTGITEICLNGNLKPEEAKVYEDEKRIICF (SEQ ID NO: 8) **FIG. 4**

CACGCGTCCGACTTGCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTGTGT
GTGCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGGTACAGAGCAAG
GGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCGCAGATGCCTACGT
GGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCAGTGAGCAGGTATACCCAGCAGCTGCGACACCATCTG
GGCCGTGACTCCAAGTTCGTGCTGTGCTATGCCCAGAAGGAGGAGCTGCTGCTGGAGGA
GATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGGGCAGCC
TGAACAGCCTGGCCTGCCTCCTGGACCACACCACCGGCATCCTCAATGAGCAGGGTGAG
ACCATCTTCATCCTGGGTGATGCTGGGGTGGGCAAGTCCATGCTGCTACAGCGGCTGCA
GAGCCTCTGGGCCACGGGCCGGCTAGACGCAGGGGTCAAATTCTTCTTCCACTTTCGCT
GCCGCATGTTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTC
AAGCACTACTGCTACCCAGAGCGGGACCCCGAGGAGGTGTTTGCCTTCTGCTGCGCTT
CCCCACGTGGCCCTCTTACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTGGACC
TGAGCCGCGTGCCTGACAGCTCCTGCCCCTGGGAGCCTGCCACCCCCCTGGTCTTGCTG
GCCAACCTGCTCAGTGGGAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCGCAC
AGGCATCGAGGTCCCGCGCCAGTTCCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCC
CCAGCCACCTGCGCGCCTATGCCAGGAGGATGTTCCCCGAGCGGGCCCTGCAGGACCGC
CTGCTGAGCCAGCTGGAGGCCAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCTCTT
CTGCTGGATCATCTTCCGGTGCTTCCAGCACTTCCGTGCTGCCTTTGAAGGCTCACCAC
AGCTGCCCCGACTGCACGATGACCCTGACAGATGTCTTCTCCTGGTCACTGAGGTCCAT
CTGAACAGGATGCAGCCAGCAGCCTGGTGCAGCGGAACACACGAGCCAGTGGAGAC
CCTCCACGCCGGCCGGGACACTCTGTGCTCGCTGGGGCAGGTGGCCACCGGGGCATGG
AGAAGAGCCTCTTTGTCTTCAACCAGGAGGAGGTGCAGGCCTCCGGGCTGCAGGAGAGA
GACATGCAGCTGGGCTTCTTGCGGGCTTTCGGGAGCTGGGCCCCGGGGTGACCAGCA
GTCCTATGAGTTTTTCCACCTCAGCCTCCTCACCTGTAAACTGGGATCCCAGTATAGA
CTTTGGAAATCAGTAGACACCATATGCTTCAAAAAACAGGGGCTATTAAATGACATCA
GGAGCCAGAAAGTCTCATGGCTGTGCTTCTTGAAGTTTATACAACAACCAGATCAC
CGATGTGCGGAGCCAGACTGGGAAAAAACAATAACAAGTGAAGGAGGGAAGTATCTCG
CCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTGGGATGTGGGGCAATCAAGTT
GGGGATGAAGGAGCAAAGCCTTCGCAGAGGCTCTGCGGAACCACCCAGCTTGACCAC
CCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCTTGCGAGGGCCC
TGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACTCAACGATGAA
GTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCATTTATGGCT
TATCCAGAATCAGATCACAGTCTTTTGTGTGCTGCTTAAAGGGGCTGCGCAGGCGG
GACTATCAGGAGTCCACTGCCTCCATGATGCAAGCCAGCTTCTGTGCAGAAAGTCTGG
TCGGCAAACTCCCTAAGTACCCGCTACAATTCTGCAGAAAAAGAATGTGTCTTGCAGC
TGTTGTAGTTACAGTAAATACACTGTGAAGAGACTTTATTGCCTATTATAATTATTTT
ATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACAGAGGAGGCCAGCCTCACCTCATTC
CAACACCTGCCATAGGGACCAACGGGAGCGAGTTGGTCACCGCTCTTTTCATTGAAGAG
TTGAGGATGTGGCACAAGTTGGTGCCAAGCTTCTTGAATAAAACGTGTTTGATGGATT
AGTATTATACCTGAAATATTTTCTTCTCTCAGCACTTTCCCATGTATTGATACTGGT
CCCCTTCACAGCTGGAGACACCGGAGTATGTGCAGTGTGGGATTTGACTCCTCCAAGG
TTTTGTGGAAGTTAATGTCAAGGAAAGGATGCACCACGGGCTTTTAATTTTAATCCTG
GAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAGCTCTTAGCTGGTCTAAGA
ATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTCCTCTGCTAGGCTACCCT
CCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTGGGAAGAAGTGATTCTG
TCCCTCCAAAGAAATAGGGCATGGCTTGCCCCCTGTGGCCCTGGCATCCAAATGGCTGCT
TTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCTGCTCCCAAGCAGCTGAAG
GGTGAATAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAAGTGGGCCAGCAGAGCAT
GTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAGGGTGGGGGTGAT
ACTACTAGATCACTTGTCTCTTGGCAGCTCATTTGTTAATAAAATACTGAAAACACAA
AA
AAAAAAAAAAAAA (SEQ ID NO: 25)

FIG. 5

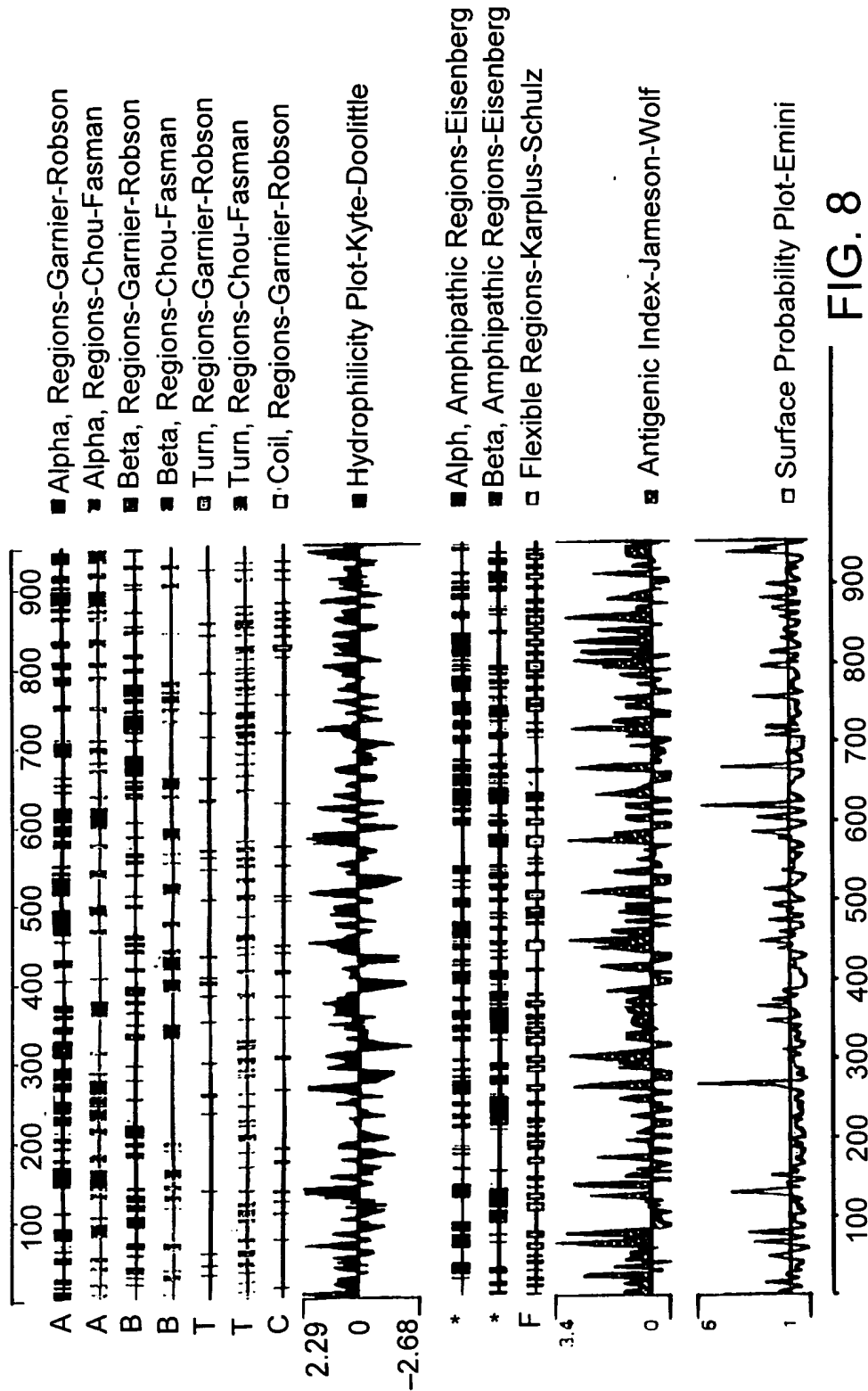
HASDLLKNDYFSAEDAEIVCACPTQPDQKVRKIILDLVQSKGEEVSEFFLYLL
QQLADAYVDLRPWLLLEIGFSPSLLTQSKVVVNTDPVSRYTQQLRHHLGRDS
KFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSLACLDDHTTGILN
EQGETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFHFRCRMFSCFK
ESDRCLQDILLFKHYCYPERPDEEVFAFLRRFPHVALFTFDGLDELHSDLD
LSRVPDSSCPWEPAHPLVLLANLLSGKLLKGASKLLTARTGIEVPRQFLRK
KVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSVPLFCWI
IFRCFQHFRAAFEGSPQLPDCTMTLTLDVFLLVTEVHLNRMQPSLVQRNTR
SPVETLHAGRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFL
RALPELGPGGDQQSYEFFHLSLLTCKTGIPV (SEQ ID NO: 26)

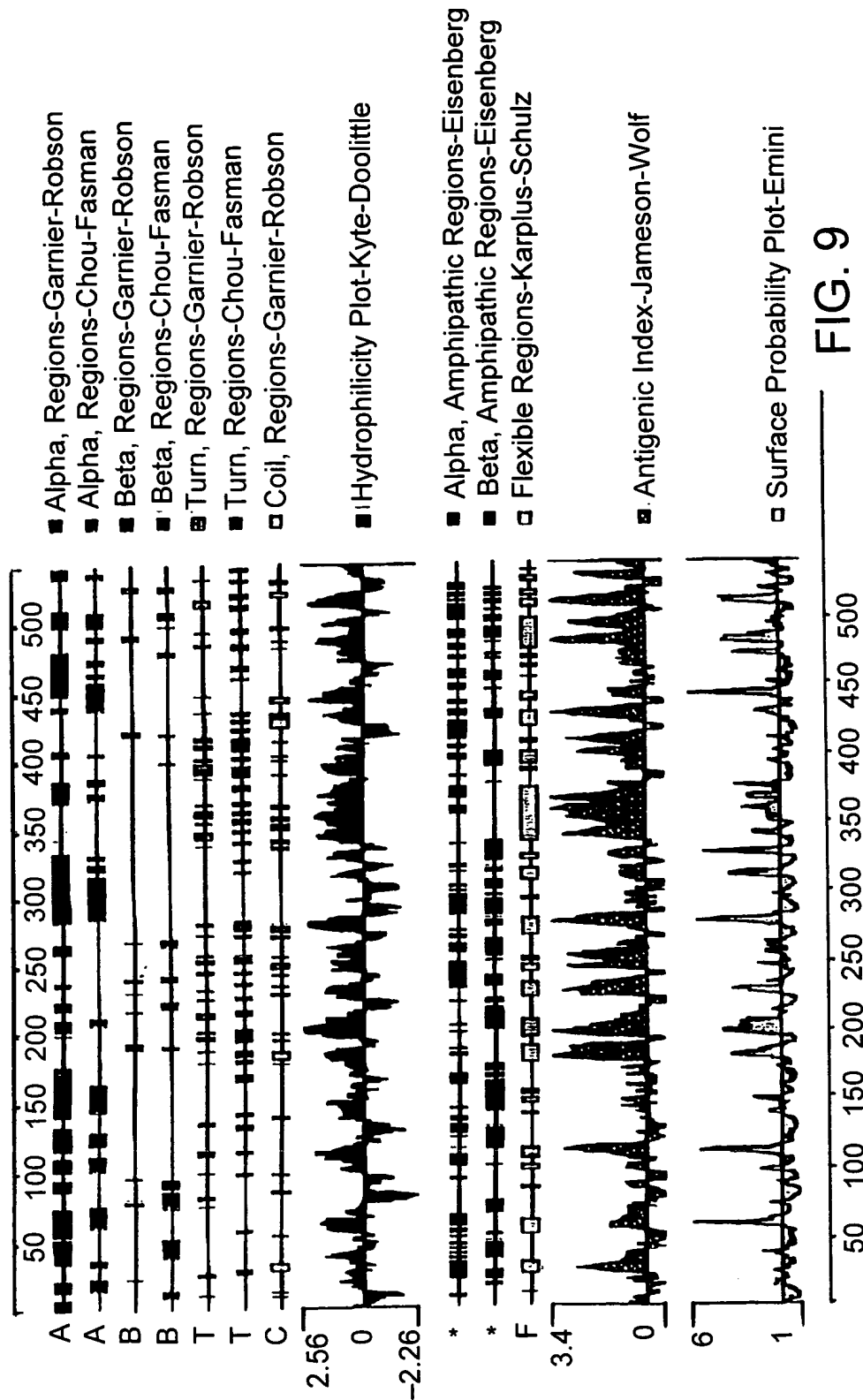
FIG. 6

SEQ. ID NO. 31/32/33/34

1	E	S	H	P	H	I	-	-	Q	L	L	K	S	N	R	E	L	L	V	T	H	I	R	N	T	Q	C	L	-	-	-	V	D	N	L	L	K	N	D	Y	CARD4-CARD		
1	L	-	Q	P	G	I	A	Q	Q	W	I	I	Q	S	K	R	E	D	I	V	N	Q	M	T	E	A	-	C	L	N	Q	S	L	D	A	L	L	S	R	D	L	CARD3-CARD	
1	A	Q	E	R	-	-	-	P	S	E	T	I	D	R	E	R	K	R	L	V	E	T	L	Q	A	D	S	-	G	L	I	-	-	L	D	A	L	L	A	R	G	V	ARC-CARD
1	M	A	S	D	D	L	S	-	-	L	I	R	K	N	R	M	A	L	F	Q	Q	L	T	-	-	-	-	C	V	L	P	I	L	D	N	L	L	K	A	N	V	CIAP1-CARD	
1	K	E	S	N	D	L	L	-	-	L	I	R	K	N	R	M	A	L	F	Q	H	L	T	-	-	-	-	C	V	I	P	I	L	D	S	L	L	T	A	G	I	CIAP2-CARD	
36	F	S	A	E	D	A	E	I	V	C	A	C	P	T	Q	P	D	K	V	R	K	I	L	D	L	V	Q	S	K	G	E	E	V	S	E	F	F	L	Y	L	CARD4-CARD		
39	I	M	K	E	D	Y	E	L	V	S	T	K	P	T	R	T	S	K	V	R	Q	L	L	D	T	T	D	I	Q	G	E	E	F	A	K	V	I	V	Q	K	CARD3-CARD		
37	L	T	G	P	E	Y	E	A	L	D	A	L	P	D	A	E	R	R	V	R	L	L	L	L	V	Q	G	K	G	E	A	A	C	Q	E	L	L	R	C	ARC-CARD			
36	I	N	K	Q	E	H	D	I	I	K	Q	K	T	Q	I	P	L	Q	A	R	E	L	I	D	T	I	W	V	K	G	N	A	A	A	A	N	I	F	K	N	C	CIAP1-CARD	
36	I	N	E	Q	E	H	D	V	I	K	Q	K	T	Q	T	S	L	Q	A	R	E	L	I	D	T	I	L	V	K	G	N	I	A	A	T	V	E	R	N	S	CIAP2-CARD		
76	L	Q	Q	L	A	D	A	Y	V	D	L	R	P	W	-	-	L	L	E	I	G	F	S	P	S	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CARD4-CARD	
79	L	K	D	N	K	Q	-	-	M	G	L	Q	P	Y	P	E	I	L	V	S	R	S	P	S	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CARD3-CARD	
77	A	Q	R	T	A	G	A	P	D	P	A	W	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ARC-CARD		
76	L	K	E	I	D	S	T	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP1-CARD		
76	L	Q	E	A	E	A	V	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CIAP2-CARD		

FIG. 7





CCCGCGTCCGCGTCCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCT
GCGAAGTCTGTNAACCTGGTGGCCAAGTGATTGTAAGTCAGGAGACTTTTCCTTCGGTTTC
TGCCTTTGATGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAACATCTGGGAAGAC
AAGTTGCTGTTTTTATGGGAATCGCAGGCTTGGAAGAGACAGAAGCAATTCAGAAATAA
ATTGGAAATTGAAGATTTAAACAATGTTGTTTTAAATATTCTAACTTCAAAGAATGATG
CCAGAACTTAAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCTGGAGGGCGCGGCCTGAAT
CCTGATTGCCCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGC
CGCTTGCTACTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAG
AGTCTCACCCCCACATTTCAATTACTGAAAAGCAATCGGGAACTTCTGGTCACTCACATCC
GCAATACTCAGTGTCTGGTGGACAACTTGCTGAAGAATGACTACTTCTCGGCCGAAGATG
CGGAGATTGTGTGTGCCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGG
TACAGAGCAAGGGCGAGGAGGTGTCCGAGTTCTTCCTCTACTTGCTCCAGCAACTCGCAG
ATGCCTACGTGGACCTCAGGCCTTGCTGCTGGAGATCGGCTTCTCCCCTTCCCTGCTCA
CTCAGAGCAAAGTCGTGGTCAACACTGACCCAGTGAGCAGGTATACCCAGCAGCTGCGAC
ACCATCTGGGCCGTGACTCCAAGTTCGTGCTGTGCTATGCCCAGAAGGAGGAGCTGCTGC
TGGAGGAGATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGG
GCAGCCTGAACAGCCTGGCCTGCCTCCTGGACCACACCACCGGCATCCTCAATGAGCAGG
CTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTCAAGCACTACTGCTA
CCCAGAGCGGGACCCCGAGGAGGTGTTTGCTTCTGCTGCGCTTCCCCACGTGGCCCT
CTTACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTGACCTGAGCCGCGTGCCTGA
CAGCTCCTGCCCCCTGGGAGCCTGCCCACCCCCTGGTCTTGCTGGCCAACCTGCTCAGTGG
GAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCGCACAGGCATCGAGGTCCCGCG
CCAGTTCCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCCCAGCCACCTGCGCGCCTA
TGCCAGGAGGATGTTCCCCGAGCGGGCCCTGCAGGACCGCCTGCTGAGCCAGCTGGAGGC
CAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCTCTTCTGCTGGATCATCTTCCGGTG
CTTCCAGCACTTCCGTGCTGCCTTTGAAGGCTCACCACAGCTGCCCCACTGCACGATGAC
CCTGACAGATGTCTTCTCCTGGTCACTGAGGTCCATCTGAACAGGATGCAGCCCAGCAG
CCTGGTGCAGCGGAACACACGCAGCCCAGTGAGACCCTCCACGCCGGCCGGGACACTCT
GTGCTCGCTGGGGCAGGTGGCCCAACGGGGCATGGAGAAGAGCCTCTTTGTCTTCACCCA
GGAGGAGGTGCAGGCCTCCGGGCTGCAGGAGAGAGACATGCAGCTGGGCTTCTGCGGGC
TTTGCCGAGCTGGGCCCCGGGGGTGACCAGCAGTCCTATGAGTTTTTCCACCTCACCT

FIG. 10A

CCAGGCCTTCTTTACAGCCTTCTTCCTCGTGCTGGACGACAGGGTGGGCACTCAGGAGCT
GCTCAGGTTCCTCCAGGAGTGGATGCCCCCTGCGGGGGCAGCGACCACGTCCTGCTATCC
TCCCTTCCTCCCGTTCCAGTGCCTGCAGGGCAGTGGTCCGGCGCGGGAAGACCTCTTCAA
GAACAAGGATCACTTCCAGTTCACCAACCTCTTCCTGTGCGGGCTGTTGKCCAAAGCCAA
ACAGAAACTCCTGCGGCATCTGGTGCCCGCGGCAGCCCTGAGGAGAAAGCGCAAGGCCCT
GTGGGCACACCTGTTTTCCAGCCTGCGGGGCTACCTGAAGAGCCTGCCCCGCGTTCAGGT
CGAAAGCTTCAACCAGGTGCAGGCCATGCCCACGTTTCATCTGGATGCTGCGCTGCATCTA
CGAGACACAGAGCCAGAAGGTGGGGCAGCTGGCGGCCAGGGGCATCTGCGCCAACTACCT
CAAGCTGACCTACTGCAACGCCTGCTCGGCCGACTGCAGCGCCCTCTCCTTCGTCCTGCA
TCACTTCCCCAAGCGGCTGGCCCTAGACCTAGACAACAACAATCTCAACGACTACGGCGT
GCGGGAGCTGCAGCCCTGCTTCAGCCGCCTCACTGTTCTCAGACTCAGCGTAAACCAGAT
CACTGACGGTGGGGTAAAGGTGCTAAGCGAAGAGCTGACCAAATACAAAATTGTGACCTA
TTTGGGTTTATACAACAACCAGATCACCGATGTCGGAGCCAGGTACGTCACCAAAATCCT
GGATGAATGCAAAGGCCTCACGCATCTTAAACTGGGAAAAAACAAAATAACAAGTGAAGG
AGGGAAGTATCTCGCCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTTGGGATGTG
GGGCAATCAAGTTGGGGATGAAGGAGCAAAGCCTTCGCAGAGGCTCTGCGGAACCACCC
CAGCTTGACCACCCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCT
TGCGAGGGCCCTGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACT
CAACGATGAAGTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCA
TTTATGGCTTATCCAGAATCASATCACAGCTWARGGGACTGCCCAGCTGGCAGATGCGTT
ACAGAGCAACACTGGCATAACAGAGATTTGCCTAAATGGAAACCTGATAAAACCAGAGGA
GGCCAAAGTCTATGAAGATGAGAAGCGGATTATCTGTTTCTGAGAGGATGCTTTCCTGTT
CATGGGGTTTTTGGCCCTGGAGCCTCAGCAGCAAATGCCACTYTGGGCAGTCTTTTGTGTC
AGTGTCTTAAAGGGGCTGCGCAGGCGGGACTATCAGGAGTCCACTGCCTCCATGATGCA
AGCCAGCTTCCTGTGCAGAAGGTCTGGTCGGCAAACCTCCCTAAGTACCCGCTACAATTCT
GCAGAAAAAGAATGTGTCTTGCGAGCTGTTGTAGTTACAGTAAATACACTGTGAAGAGAC
TTTATTGCCTATTATAATTATTTTTATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACA
GAGGAGGCCAGCCTCACCTCATTCACACCTGCCATAGGGACCAACGGGAGCGAGTTGG
TCACCGCTCTTTTCATTGAAGAGTTGAGGATGTGGCACAAAGTTGGTGCCAAGCTTCTTG
AATAAAACGTGTTTGATGGATTAGTATTATACCTGAAATATTTTCTTCCTTCTCAGCACT
TTCCCATGTATTGATACTGGTCCCACTTCACAGCTGGAGACACCGGAGTATGTGCAGTGT
GGGATTTGACTCCTCCAAGGTTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGG

FIG. 10B

GCTTTTAATTTTAATCCTGGAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAG
CTCTTAGCTGGTCTAAGAATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTC
CTCTGCTAGGCTACCCTCCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTG
GGAAGAAGTGATTCTGTCCCTCCAAAGAAATAGGGCATGGCTTGCCCCTGTGGCCCTGGC
ATCCAAATGGCTGCTTTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTC
CCAAGCAGCTGAAGGGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAACTGG
GCCAGCAGAGCATGTTGGACACCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAG
GGTGGGGGTGATACTACTAGATCACTTGTCTCTTGCCAGCTCATTGTTAATAAAATAC
TGAAAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGG (SEQ ID NO:39)

FIG. 10C

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLEIGFSPSLLTQSKVV
VNTDPVSRYTQQLRHHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLSL
ACLLDHTTGILNEQAASRKVTGCVCRTCSSSTTATQSGTPRRCLPSCCASPTWPSSPSMA
WTSCRTWT (SEQ ID NO:40)

FIG. 11

CACGCGTCCGCGCTACTGCGGGAGCAGCGTCCTCCCGGGCCACGGCGCTTCCCGGCCCCG
GCGTCCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCTGCGAAGTCT
GTAAACCTGGTGGCCAAGTGATTGTAAGTCAGGAGACTTTCCTTCGGTTTCTGCCTTTGA
TGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAAATCTGGGAAGACAAGTTGCTG
TTTTTATGGGAATCGCAGGCTTGAAGAGACAGAAGCAATTCCAGAAATAAATTGGAAAT
TGAAGATTTAAACAATGTTGTTTTTAAATATTCTAACTTCAAAGAATGATGCCAGAACT
TAAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCTGGAGGGCGCGGCCTGAATCCTGATTGC
CCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGCCGCTTGCTA
CTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAGAGTCTCACC
CCCACATTCAATTACTGAAAAGCAATCGGGAACCTTCTGGTCACTCACATCCGCAATACTC
AGTGTCTGGTGGACAACCTTGTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTG
TGTGTGCCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGGTACAGAGCA
AGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCGCAGATGCCTACG
TGGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCCAGGTAGGAGTCAGCCCCAGCAAGACCGCAGGCACCAGT
GCAAGCAGGGCCCTGGGGGGTTTGGTAATGGCTGGGCCAGCCCTGAGTGCCACCTCAGGA
AGCAGGCCCCAGGTGCTATTTTGAATTTTAGAAAGGAACAGCTGAATCCTGTCTCCCAAGTG
CAGCCCAGGTGGCTGCGATTGAACTGCCCCACACCTCGATGGTCTGGTTTATAGAGGGGCC
TTTGGAAGTATGGGAATGGCCTGTGTTCTGACCCCTTGCTTTCTTCTTCTTCTGACATAT
GTAGACATTTTAATGGTTGCACAAATTCAGGTTGTATTTTTTTTTCTTTAAAAAATCT
TTAGCTGGACATGGTAGCACACACCTGTAGTTCAGCTACTCAGGAGGCTGAGGCAAGAG
GACTGCTTGAGCCCCAGAGTCTAAGGCTGCAGCGAGCTATGATTGTGCCCCTACACTCCA
CAGCCTGGGTTTTTAGAGTGAGACCCTGTCTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAANGGGCGG (SEQ ID NO:41)

FIG. 12

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLEIGFSPSLLTQSKVV
VNTDPGRSQPQDRRHQCKQGPGGFGNGWASPECHLRKQAQVLF
(SEQ ID NO:42)

FIG. 13

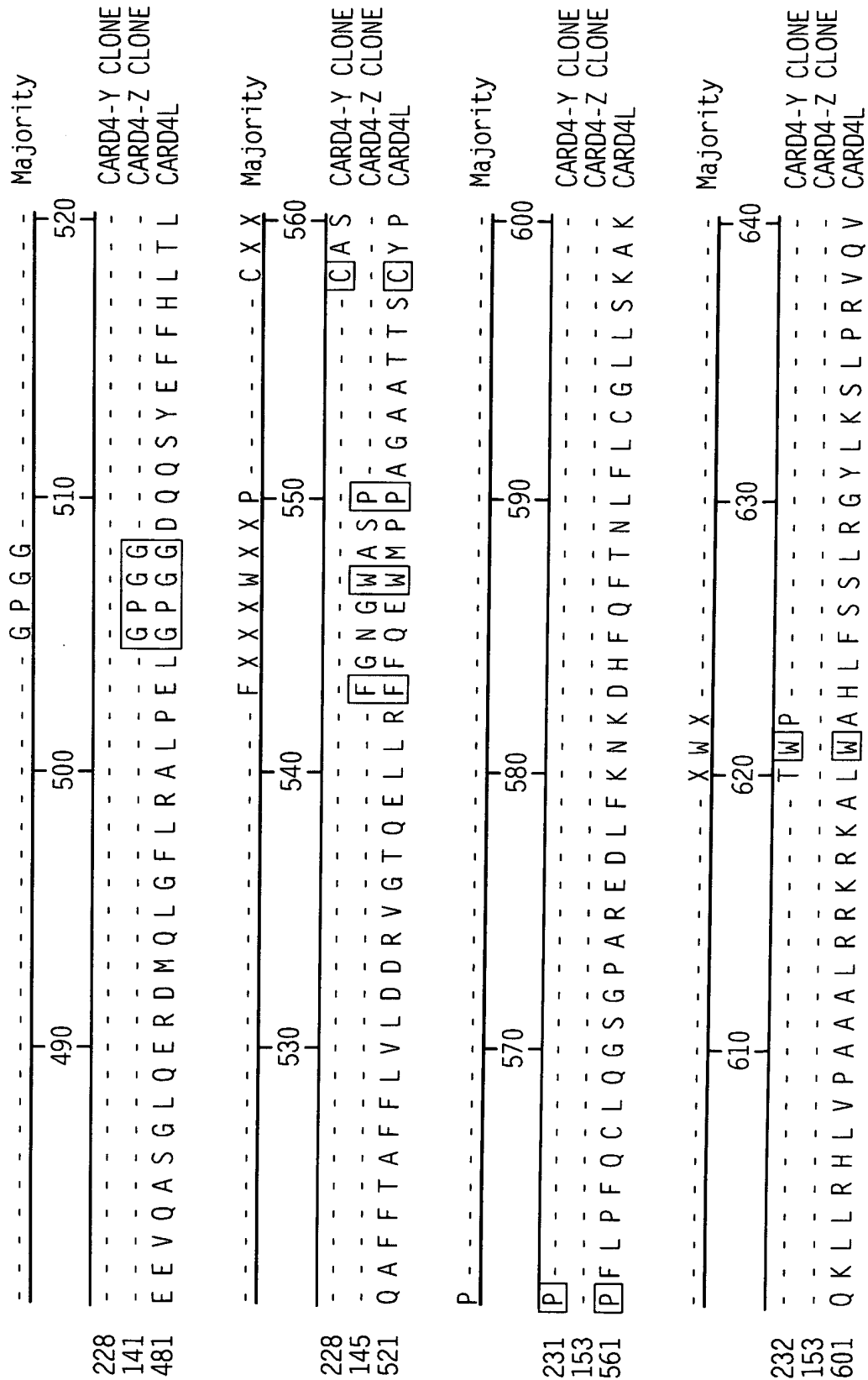
	M E E Q G H S E M E I I P S E S H P H I Q L L K S N R E L L V T H I R N T Q C L	Majority
	10203040	
1	M E E Q G H S E M E I I P S E S H P H I Q L L K S N R E L L V T H I R N T Q C L	CARD4-Y CLONE
1	M E E Q G H S E M E I I P S E S H P H I Q L L K S N R E L L V T H I R N T Q C L	CARD4-Z CLONE
1	M E E Q G H S E M E I I P S E S H P H I Q L L K S N R E L L V T H I R N T Q C L	CARD4L
	V D N L L K N D Y F S A E D A E I V C A C P T Q P D K V R K I L D L V Q S K G E	Majority
	50607080	
41	V D N L L K N D Y F S A E D A E I V C A C P T Q P D K V R K I L D L V Q S K G E	CARD4-Y CLONE
41	V D N L L K N D Y F S A E D A E I V C A C P T Q P D K V R K I L D L V Q S K G E	CARD4-Z CLONE
41	V D N L L K N D Y F S A E D A E I V C A C P T Q P D K V R K I L D L V Q S K G E	CARD4L
	E V S E F F L Y L L Q Q L A D A Y V D L R P W L L E I G F S P S L L T Q S K V V	Majority
	90100110120	
81	E V S E F F L Y L L Q Q L A D A Y V D L R P W L L E I G F S P S L L T Q S K V V	CARD4-Y CLONE
81	E V S E F F L Y L L Q Q L A D A Y V D L R P W L L E I G F S P S L L T Q S K V V	CARD4-Z CLONE
81	E V S E F F L Y L L Q Q L A D A Y V D L R P W L L E I G F S P S L L T Q S K V V	CARD4L
	V N T D P V S R Y T Q Q L R H H L G R D S K F V L C Y A Q K E E L L E E I Y M	Majority
	130140150160	
121	V N T D P V S R Y T Q Q L R H H L G R D S K F V L C Y A Q K E E L L E E I Y M	CARD4-Y CLONE
121	V N T D P G R S Q P Q Q D R R H H L G R D S K F V L C Y A Q K E E L L E E I Y M	CARD4-Z CLONE
121	V N T D P V S R Y T Q Q L R H H L G R D S K F V L C Y A Q K E E L L E E I Y M	CARD4L

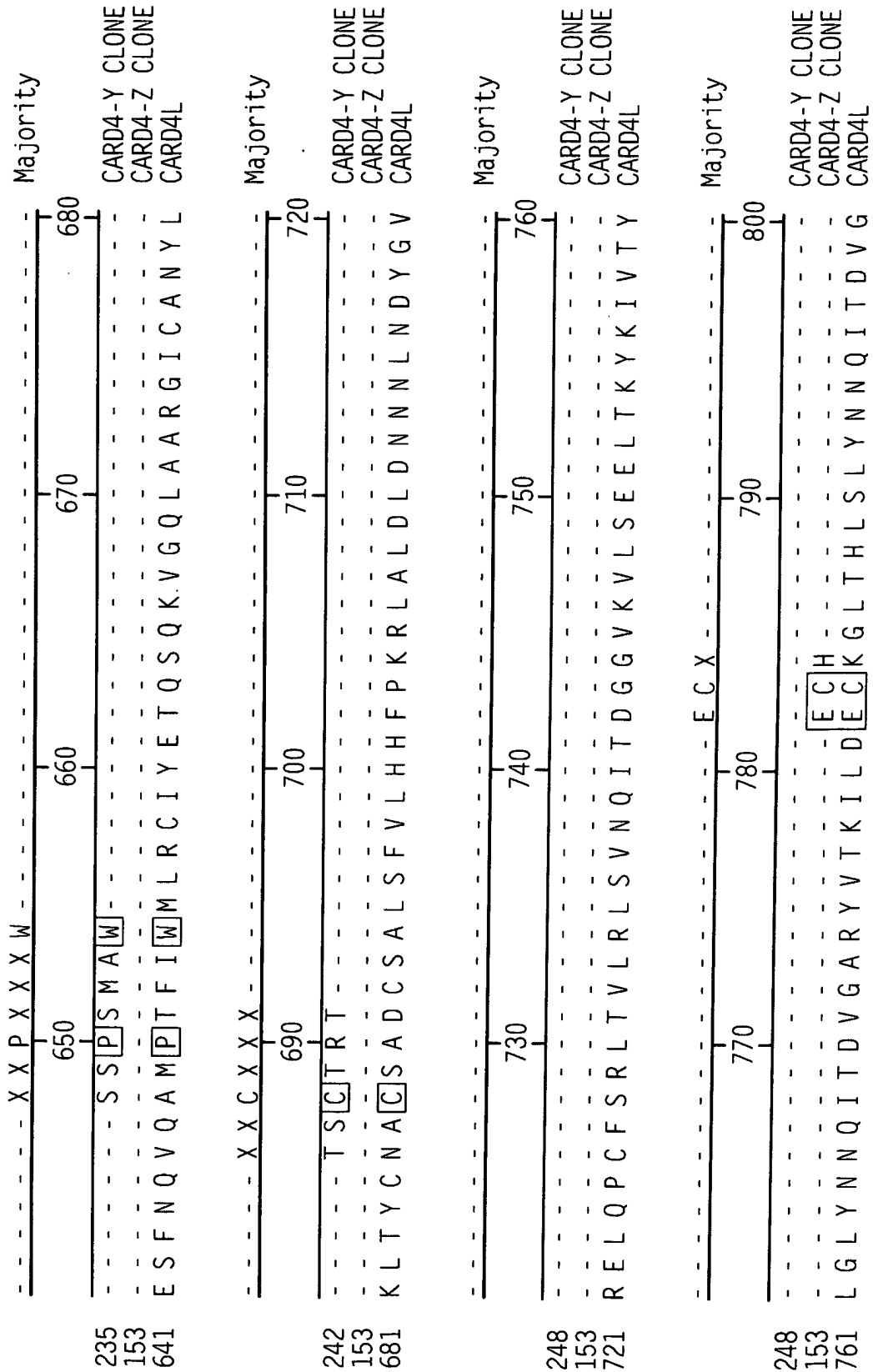
FIG. 14A

FIG. 14B

212	- - - - - T X X T X X X X P R - - - - -	Majority	- - - - -
141	- - - - - 330 - - - - - 340 - - - - - 350 - - - - - 360		
321	- - - - - T T A T Q S G T P R - - - - -	CARD4-Y CLONE	- - - - -
	- - - - - K L L G A S K L L T A R T G I E V P R Q F L R K K V L L R G F S P S H L R A Y	CARD4-Z CLONE	- - - - -
		CARD4L	- - - - -
222	- - - - -	Majority	- - - - - R C
141	- - - - - 370 - - - - - 380 - - - - - 390 - - - - - 400		
361	- - - - - A R M F P E R A L Q D R L L S Q L E A N P N L C S L C S V P L F C W I I F R C	CARD4-Y CLONE	- - - - - R C
		CARD4-Z CLONE	- - - - -
		CARD4L	- - - - -
224	- - - - -	Majority	- - - - -
141	- - - - - 410 - - - - - 420 - - - - - 430 - - - - - 440		
401	- - - - - F Q H F R A A F E G S P Q L P D C T M T L T D V F L L V T E V H L N R M Q P S S	CARD4-Y CLONE	- - - - -
		CARD4-Z CLONE	- - - - -
		CARD4L	- - - - -
228	- - - - -	Majority	- - - - -
141	- - - - - 450 - - - - - 460 - - - - - 470 - - - - - 480		
441	- - - - - L V Q R N T R S P V E T L H A G R D T L C S L G Q V A H R G M E K S L F V F T Q	CARD4-Y CLONE	- - - - -
		CARD4-Z CLONE	- - - - -
		CARD4L	- - - - -

FIG. 14C





[illegible]

	X	X	X	X	F		Majority
249							
164	-	-	-	-	F		CARD4-Y CLONE
961	R	I	I	C	F		CARD4-Z CLONE
							CARD4L

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 14G

CCACGCGTCCGCGGACCGCGAGCGGTAGCGCCCTCCCTCCCAGCTGTTGTCCCGCCCGAT
CCGCGACCCTAGTCCCCGGATCCCCTTGCTGAGAGTCACCGTACTCCAGGGCCAACTGAG
CCAAAGTCCTGCCAACTTGGGTGAGCAATGAAAGGCAGGATCCTGGGTGGTGGCCCTGAA
TCCTGATTTGTCTGCCCTGCCAGCGAGACACATGTGGTCAAAGATGAATTTGAGAAAAGT
AGCTGCTGGCTACTTGAACAATGGAGGAACACGGCCATCATGAGATGGAAGGCACCCCAT
TGGGTGTCACTCCCACATTAACTGCTGAAGATCAACAGGGAACATCTGGTCACCAACA
TTCGGAACACTCAGTGTCTGGTGGACAACTTGCTGGAGAATGGCTACTTCTCAGCCGAAG
ATGCAGAGATTGTGTGTGCCTGTCCCACCAAGCCTGACAAGGTCCGAAAGATCCTTGACC
TGGTGCAGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCTCTACGTGCTGCAGCAGCTGG
AGGATGCTTACGTGGACCTCAGGCTGTGGCTCTCAGAAATTGGCTTCTCCCCTTCCCAGC
TCATTTCGGACCAAACACTATCGTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGC
GACACCAACTGGGCCGCGACTCCAAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTGC
TGCTGGAGGAGACCTATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACC
TGGGCAGCCTAGGAGGCCTGGATTGCCTGCTGGACCACAGTACGGGCGTCCTCAACGAGC
ATGGCGAGACTGTCTTCGTGTTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGA
GGTTGCAGAGCCTCTGGGCGTCAGGCAGGTTGACCTCCACAGCCAAATTCTTCTTCCACT
TCCGCTGCCCGCATGTTTCAAGTCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTGC
TCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTGC
GCTTTCCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTCG
ACCTGAGCCGCGTGCCGGATAGCTGCTGCCCCTGGGAGCCGGCTCACCTCTGGTCCTGC
TGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCTCGCA
CAGGCGTGGAGGTCCCCCGCCAGCTCCTGCGCAAAAAGGTGCTGCTCCGGGGCTTCTCCC
CAAGTCACCTGCGCGCCTATGCCCCGCGGATGTTCCCCGAGCGCACAGCGCAGGAGCATC
TGCTGCAGCAGCTGGATGCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCT
GTTGGATCATCTTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCAC
AGTTGCCGGAAGTGTGCTGTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATC
TGAACAGGCCGCGAGCCAGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGCGGAAACCC
TACGTGCAGGCTGGCGCACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACA
AGAGCCTCTTTGTGTTTGGCCAGGAGGAGGTGCAGGCGTCGAAGCTGCAGGAAGGAGATC
TGCAGCTGGGCTTCTGCGGGCTTTGCCCGATGTGGGCCCTGAGCAGGGCCAGTCTTACG
AATTTTCCACCTTACGCTCCAGGCCTTCTTACCGCCTTCTTCTTGGTAGCAGATGACA
AAGTGAGCACCCGGGAGTTGCTGAGGTTCTTTCGAGAATGGACGTCTCCTGGAGAGGCAA

FIG. 15A

CAAGCTCGTCCTGCCATTCTTCCTTCTTCTCCTTCCAGTGCCTGGGCGGCAGAAGCCGGT
TGGGCCCTGATCCTTTTCAGGAACAAAGATCACTTCCAGTTCACCAACCTCTTCGTGTGCG
GGCTACTGGCCAAAGCCCGACAGAACTCCTTCGGCAGCTGGTGCCCAAGGCTATCCTGA
GGAGGAAGCGCAAGGCCCTGTGGGCTCACCTGTTTGCTAGCCTGCGCTCCTACTTGAAGA
GCCTACCTCGGGTCCAGTCTGGAGGCTTTAACCAGGTGCATGCCATGCCACATTCTGT
GGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCCGCCAGGG
GCATCAGTGCGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGACTGCAGCG
CCCTGTCCTTCGTCTGTCATCACTTCCACAGGCAGCTGGCCCTAGACCTGGACAACAACA
ACCTCAATGACTATGGCGTGCAGGAGCTGCAGCCTTGCTTTAGCCGTCTCACGGTTATCA
GACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAGGTGCTATGTGAGGAACTGACCA
AGTATAAGATCGTGACGTTCTTGGGTTTATACAACAACCAGATAACTGATATCGGAGCCA
GGTATGTGGCCCAAATCCTGGATGAATGCAGAGGCCTCAAGCACCTTAAACTAGGGAAAA
ACAGAATAACAAGTGAGGGCGGGAAGTGTGTGGCTTTGGCTGTGAAGAACAGCACCTCCA
TCGTTGATGTTGGGATGTGGGGTAATCAGATTGGAGACGAAGGGGCAAAGGCCTTCGCAG
AGGCATTGAAGGACCACCCAGCCTGACCACTCTCAGTCTTGCAATTCAATGGCATCTCTC
CGGAGGGAGGGAAGAGCCTTGCGCAGGCCCTGAAGCAGAACACCACACTGACAGTAATCT
GGCTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAG
TGAACCAGACGCTACGGCATTTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACAG
CGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGAA
ACTTGATTAAGCCCGAGGAGGCCAAAGTCTTCGAGAATGAGAAGAGAATCATCTGCTTCT
GACGGACGCTCCTGGGCAGGATCTTTGTCCTAGGTTGCTCCTCAGTCACAGACAGCACTG
TGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTGCCTGTCAGGAGC
CCACACCTCCACAGTGCACACCGATGTCCCCTGCTCATGCTTGGACTGGTAGCACCCGCG
CCGCGGCTGAGACCCTGCAGACGCAGGGAGTCTTAGGAACCATCGTCACCACTCAAAGCC
AGCAGGGCATCTTCTGTACAAAGATCTCCCTGCATATCCACTAGACGGAAGCTGAAGGAA
CGCAACAGCAGAGGAGGCCAACAGACGCCTGGCTGAAGGCTCCGTGGGACCAACGGTGTG
ACCTTCAGAAAAGAGCTGGGAACTTGAGCAGAGCCGATGGTAACTTCTTGGGGAAAGAAG
GCACCCAGTGACTGCATGGTTATTCTGAGTCCTCCTTCTCTGCTTAGTCCCTCTCACTG
TACAGGTCTGTTTCTTCTCGCAGCTGTGGCTGCTGAAGTAGGTCCACTGTGGGGAGAGC
TCATCACAGACTTTGGTTTCGGTTCTGGATTCTCAGTGGTGGCAACCGAGAGTCAGACGAT
ACCCTCTAGGTCAGTCTCAGAGGATCTCTATGCTGTGAGAGGGTTGAGGGCCACCCAGA
ATTTTTTTTTTTTACCAGTTTTTACTGTGCCTGCCCCAGGAGGGAGAATTACTTCCCAGC

FIG. 15B

CTCCACAGCAGCAGGCATGGCTTGCCTCAATGGTCCTGAGATCCCAACAAAACCTCTCTCC
CTTGCCTGTGAGCAGAAAGTATCTTCATGTCCTCAGAAGTTGGAGGGTGACTGGACACAG
TTAAGACTCAGAGAGCCAGCTGATAGCTCAAAGCAAAGCATGGCACATACCCACCACCAT
ACCATGGTGCGCATGGGATGGGACAGTTGGAATGTTGCAGATAACGTGTTCTTTTGCCAG
TTCATTTGTTAATAAAAATATTTAAACGTTAAAAAAGGGCG
G (SEQ ID NO:43)

FIG. 15C

MEEHGHHEMEGTPLGCHSHIKLLKINREHLVTNIRNTQCLVDNLLENGYFSAEDAEIVCA
CPTKPKDKVRKILDLVQSKGEEVSEFFLYVLQQLDAYVDLRLWLSEIGFSPSQLIRKTI
VNTDPVSRYTQQLRHQLGRDSKFMLCYAQKEDLLEETYMDTLMGLVGNNENLGS LGGL
DCLLDHSTGVLNEHGETVFVFGDAGVGKSMMLQRLQSLWASGRLTSTAKFFFHFRCRMFS
CFKESDMLSLQDLLFKHFCYPEQDPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPD
SCCPWEPAPHLVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKVLLRGFSPSHLRAY
ARRMFPERTAQEHLQQLDANPNLCSLCGVPLFCWIIIFRCFQHFQTVFEGSSSQLPDCAV
TLTDVFLLVTEVHLNRPQPSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLFVFG
QEEVQASKLQEGDLQLGFLRALPDVGPEQGQSYEFFHLLTQAFFTAFFLVADDKVSTREL
LRFFREWTSPGEATSSSCHSSFFSFQCLGGRSRLGPD PFRNKDHFQFTNLFVCGLLAKAR
QKLLRQLVPKAILRRKRKALWAHLFASLSYLKSLPRVQSGGFNQVHAMPTFLWMLRCIY
ETQSQKVGRLAARGISADYLKLAFCNACSA DCSALS FVLHHFHRQLALDLDNNNLNDYGV
QELQPCFSRLTVIRLSVNQITDTGVKVLCEELTKYKIVTFLGLYNNQITDIGARYVAQIL
DECRGLKHLKLGNRITSEGGKCV ALAVKNSTSIVDVGMWGNQIGDEGAKAF AEALKDHP
SLTTL SLAFNGISPEGGKSLAQALKQNTTTLTVIWLTKNELNDESAECFAEMLRVNQTLRH
LWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRIICF
(SEQ ID NO:44)

FIG. 16

mCARD4Lpep . PRO	10	20	30	40	50	60	70	80	90
hCARD4Lpep . PRO	10	20	30	40	50	60	70	80	90
mCARD4Lpep . PRO	100	110	120	130	140	150	160	170	180
hCARD4Lpep . PRO	100	110	120	130	140	150	160	170	180
mCARD4Lpep . PRO	190	200	210	220	230	240	250	260	270
hCARD4Lpep . PRO	190	200	210	220	230	240	250	260	270
mCARD4Lpep . PRO	280	290	300	310	320	330	340	350	360
hCARD4Lpep . PRO	280	290	300	310	320	330	340	350	360
mCARD4Lpep . PRO	370	380	390	400	410	420	430	440	450
hCARD4Lpep . PRO	370	380	390	400	410	420	430	440	450
mCARD4Lpep . PRO	460	470	480	490	500	510	520	530	540
hCARD4Lpep . PRO	460	470	480	490	500	510	520	530	540

FIG. 17A

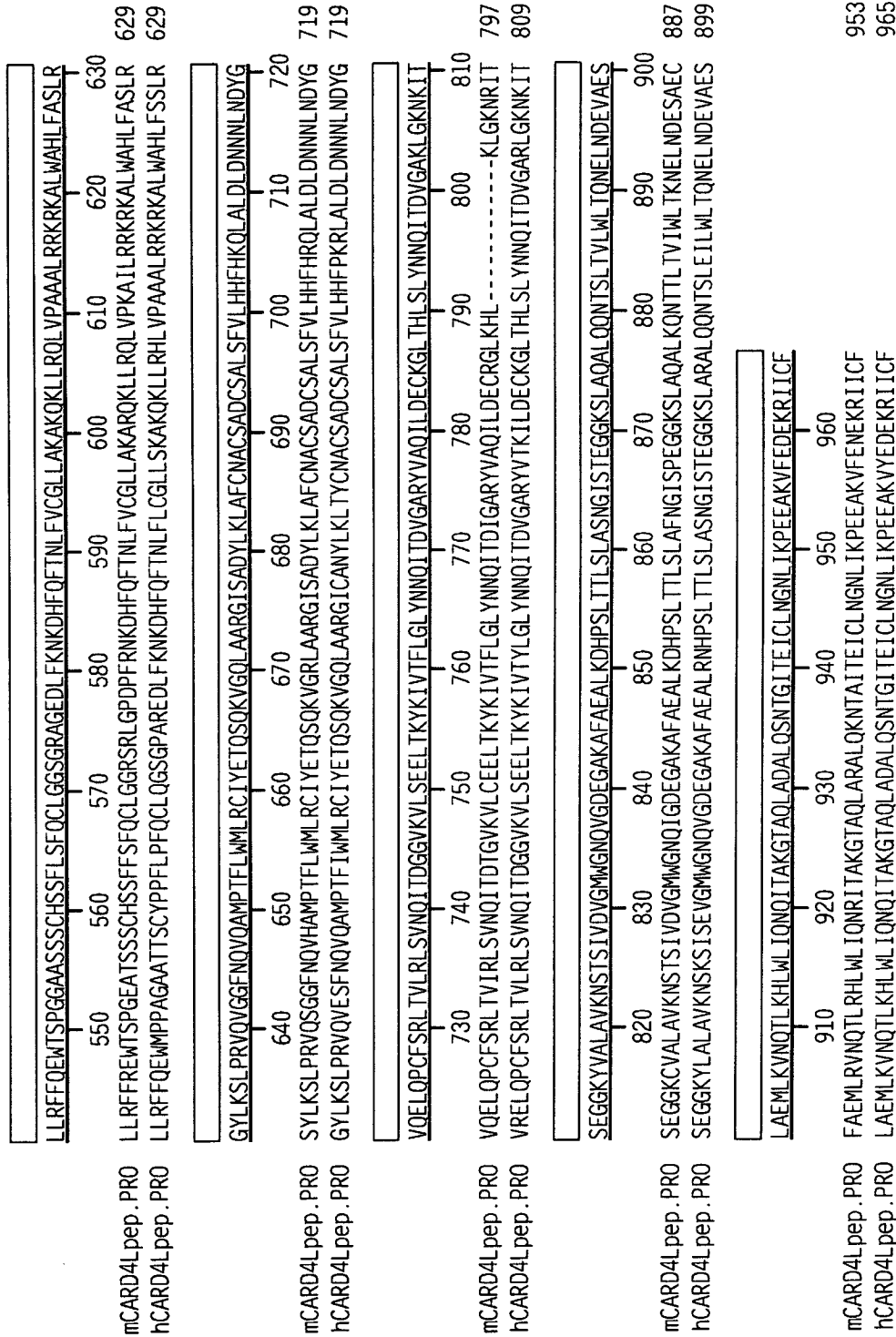


FIG. 17B

gatcatcggtcactgcagccttgaactcttgtgctcatgtgatcctcctgccttagcctcccca
tagctgggactacaggtgcgccaccatgcctggctaattttttttatttttgtagagatgggtgt
ctcactatgttgacaggttggtctcaaactactggccttacttcaagctatctacccatctcag
cctcccaaagcgctgggattacagtcagtgagccaacttgccctggccagataaagggtcttaagcat
ggttccttccctgctctaggttagagaaacccccacaaccagtgagggtggggtgagctcttctgt
agcttttgccttgcctgatgatgtcattgatctcttcaggggctgcgcagagtagcaggggcccctg
gagggcgccgctgaatcctgattgcccttctgctgagaggacacacgcagctgaagatgaattt
gggaaaagtagccgcttgctactttaactatggaagagcagggccacagtgagatggaaataatc
ccatcagagctctacccccacattcaattactgaaaagcaatcgggaaacttctggctcactcacat
ccgcaatactcagtgcttggtggacaacttgctgaagaatgactacttctcgccgaagatgcgg
agattgtgtgtgcctgccccaccagcctgacaagggtgccccggggacagggacgggcatggcat
tgtgtggaccccgaggagctagaagaggcctctccctgctgatctgagtgaagagcgtgggagttt
agtccagcggggcagggctgcattttggggactaatagcacacaaatgcctgggttagcaggttg
cacagtcaggtattttacttctgtgtttgtgtctggagcaaaccctgacatctcagttctcattg
ctgtgtgtattgggtcccagacacttcatttttagatcccctttaaattaggagggaaaaagaac
ataagcataagagcatccccagcagcagtggtcattcagtgccctctgaaggctggagggctgctt
gttgcctgggtgagactcggaggggaaccgactcaggggtcaggaatgatgacatcccacgggtgggt
ccacagtgagaatcttccccgctccactgtgggacgccttaacagcccttacttccacttacgc
tttgcggtatctcctgaaaaataaaaatggagaccacaaattccttcttggttagaggaatgacac
aactcatttatgacatgaccccgctgggactcagaagagaccaggacgggtttctgggggaagcag
tagcacactcgtgtgctttgttctcttctcttgatttgtttccacatttttaacaagaaaaaa
agccgtttttaatatatggcctatcgccctcctactgtgtggcccaggtgcctacctcattatgc
ccaaggggtggttctcacctctccactctcattcctgcacagcagttgtgtcaggttaagagggga
caaggagaaggctgggcaccgtggctcacgcctgtaatcccagcactttggggaggccgaggcagg
cagatcacctaagggtcaggagtttgagaccagcctggccaacatggggaaaaccgctctctaata
aaaacacaaaaaattagtcgggcatgggtgggtgggtgcctgtaatcccagccacttgggaggctgag
gaaagagaattccttgaacctgggaggtggaggttgagtgagccaagattgtgccattgcactc
cagccctccagcctgggtgacagagcaagactctgtctcaaaaaagaaaaaaaaaaaaaagggt
agagaagtcacatgggtatttctgtctgctcttttatttttaggctcatggaagcctcctgggttct
tagagctgagtggttttatttctgtcaggaggtcatttcacagatttccgggctccaatatgt
tgactgtcacagcagctgggggggatggcatagctaccggctgtaactaagaactcagagccctgcc
ctgagcctgcctgaggggtccttatggtaggagatgcccctcatgccagcccgctccctcatgct
tgtgtcacctccaggtccgcaaaattctggacctggtacagagcaaggcgaggaggtgtccgag
ttcttctctacttgctccagcaactcgcagatgcctacgtggacctcaggccttggctgctgga
gatcggttctccccttccctgctcactcagagcaaaagtcgtggtcaacactgacccaggtagga
gtcagccccagcaagaccgcaggcaccagtgcaagcagggccctgggggggttggttaatggctgg
gccagccctgagtgccacctcaggaagcaggcccaggtgctattttgatttttagaaaggaacagc
tgaatcctgtctccaagtgacagccaggtggctgcgattgaactgccacacctcgatggtctg
gtttatagaggggcccctttggaagtatgggaatggcctgtgttctgaccccttgctttcttccctat
tctgacatatgtagacattttaatggttgacacaaattcaagggttgatttttttttcttttaaaa
aaatcttttagctggacatggttagcacacacctgtagtccagctactcaggaggctgaggcaaga
ggactgcttgagccccagagcttaaggctgcagcagagctatgattgtgcccctacactccagcct
gggtgacagagtgagaccctgtctctaaaaaaggaaagaaaaaattaaaaagccttgccaggtt
tgattctaggcaaggtattctgtcaccgttgagtgcagtccttatttccaaactaatggaagac
cccatcagttaactgattagttcaataagtttttttgcctgtatccaccacatgccaaagacccta
cactgtgctggatgtcagggagacagtggtgagcagacacagacaggggttccctgcctcagggag
cttcaagtcagctggaagagaccaccagtcagcaatctcaaaaatgtgtcaggacagcggcagtc
caaggcatgtgagaacatatcattagggccaggatctgctctggggcaggagttctcttccctg
cttttgaaactctccactttgagacagctgttggttaacataccagcaccaaggacctaagtccctgc
cttttaagaatccaatatgttggttggaacagaagcacaagacaggtgtgtgcttaggggaaac
aaggccagccggcagagtgctcagtgctaggctccagcttccacagccctgcaggtgcctgccag
ccactgctagcttctgactctgtctgctccttccctgtctcccttggttccctcccccatgaaaa
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FIG. 18A

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FIG. 18B

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FIG. 18C

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FIG. 18D

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FIG. 18E

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FIG. 18F

gtgccgacccccagcccactgttggtgtgagcaggctgtgctgatgacccatttcccgtccagcctg
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FIG. 18G

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FIG. 18H

caccaccactgactgtgcaaggcacaacgcaggggtggtttctgtttattcctccagcaaccctgc
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FIG. 18I

tattgtgtgatacacgagtgtgtgctatgaacacaccttgggaaggagtgtgagaggatccttaa
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FIG. 18J

1 GTCGACCCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGG
CAGCTGGGTGCGCAGGCCGTCGTCCGTCCGACGTCGTCCGCTCGTTCGTTCTCATTTC

63 TGACCGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCACGAGATGCCATCCTGGACGCTCTT
ACTGGCGCCGACGGGTGGGGTCTCGGTACCCCGCCCGTGCTCTACGGTAGGACCTGCGAGAA

1 M G R A R D A I L D A L

125 GAAAACTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
CTTTTGAACAGTCCCTACTTGAGTTTTTCAAGTTCTACTTCGACGACTGTCACGTTGACGC

13 E N L S G D E L K K F K M K L L T V Q L R

187 AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCACTG
TCTTCCGATACCCGCGTAGGGTGCGCCCCGGGACGACGTCACCTGCGGTATCTAGAGTGAC

33 E G Y G R I P R G A L L Q M D A I D L T

249 ACAAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCACAATGACTGTGCTTAGA
TGTTTGAACAGTCGATGATAGACCTCAGCATACCGAACCTCGAGTGTTACTGACACGAATCT

54 D K L V S Y Y L E S Y G L E L T M T V L R

311 GACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGAAGAGTCTGGAGCTGT
CTGTACCCGAATGTCTCGACCGACTCGTCGACGTTTGCTGATTTCTTCTCAGACCTCGACA

75 D M G L Q E L A E Q L Q T T K E E S G A V

373 GGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGGACACTTTGTGGACCAGC
CCGTCGACGTCGGTCACAGGGACGAGTCTCATGTCCGTCTTGTCTGTGAAACACCTGGTCG

95 A A A A S V P A Q S T A R T G H F V D Q

435 ACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGCTGGATGCTTTGCATGGC
TGTCGTTTCGTGAGTAACGGTCCCAGTGTCTTACCTGCCTCACGACCTACGAAACGTACCG

116 H R Q A L I A R V T E V D G V L D A L H G

497 AGTGTGCTGACTGAAGGACAGTACCAGGCAGTTTCGTGCAGAGACCACGCAAGACAAGAT
TCACACGACTGACTTCCTGTCATGGTCCGTCAAGCACGTCTCTGGTGGTGGTCTCTGTTCTA

137 S V L T E G Q Y Q A V R A E T T S Q D K M

559 GAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCTGCAAGGACTCCCTCCTCCAGG
CTCCTTCGAGAAGTCGAAACAAGGTAGGACCTTGGACTGGACGTTCTGAGGGAGGAGGTCC

157 R K L F S F V P S W N L T C K D S L L Q

621 CCTTGAAGGAAATACATCCCTACTTGGTGATGGACCTGGAGCAGAGCTGAGGTATCTTTTCC
GGAACCTCCTTTATGTAGGGATGAACCACTACCTGGACCTCGTCTCGACTCCATAGAAAAGG

178 A L K E I H P Y L V M D L E Q S

683 AGCTACATTATCTAGCTCCTGACTTTGTATACACAATTTTGAACCAATTTGTATTTGT
TCGATGTAATAGATCGAGGACTGAAACATATGTGTTTAAACCTTTTGTGTTAAACATAAACA

745 GTTTAAAAAAGGGCGCGCGC
CAAATTTTTTTTTTTTTTTTTTCCCGCGCGC

FIG. 19

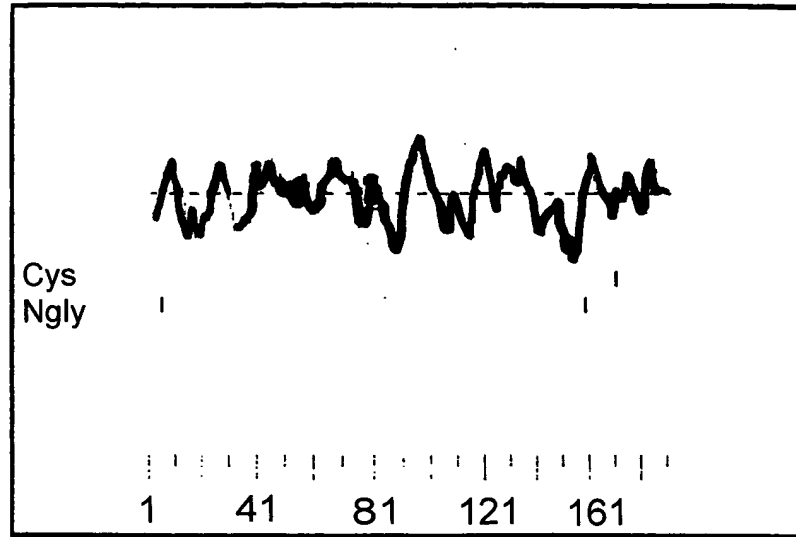


FIG. 20

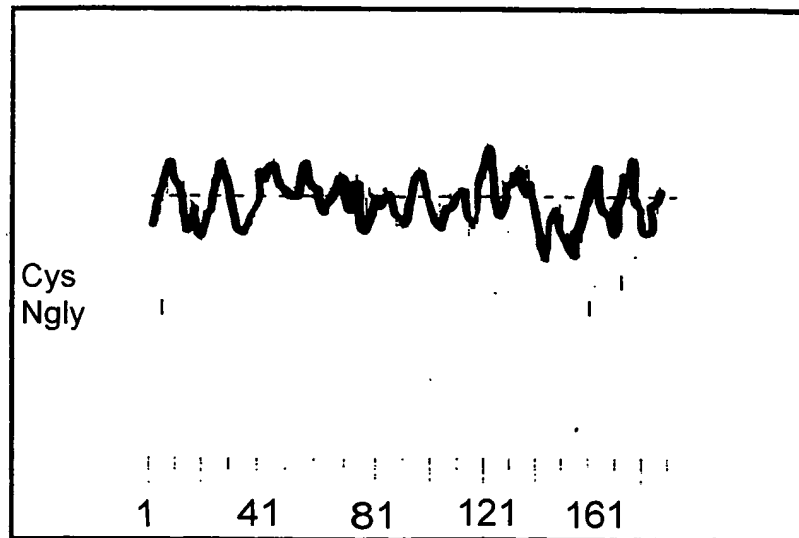


FIG. 22

1 CGCGTCCGGCTGCAGCGGGGTGAGCGGGCGCAGCGCCGGGGATCCTGGAGCCATGGGGC
CGCGAGGCCGACGTCGCCCCACTCGCCGCCGTGCGCGGCCCTAGGACCTCGGTACCCCG
1► M G

61 GCGCGCGCGACGCCATCCTGGATGCGCTGGAGAACCTGACCGCCGAGGAGCTCAAGAAGT
CGCGCGCGCTGCGGTAGGACCTACGCGACCTCTTGGAAGTGGCGGCTCCTCGAGTTCTTCA
3► R A R D A I L D A L E N L T A E E L K K

121 TCAAGCTGAAGCTGCTGTGCGGTGCCGTGCCGAGGGCTACGGGCGCATCCCGCGGGGCG
AGTTGCACTTCGACGACAGCCACGGCGACGCGCTCCCGATGCCCGCGTAGGGCGCCCCCG
23► F K L K L L S V P L R E G Y G R I P R G

181 CGCTGCTGTCCATGGACGCCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGA
GCGACGACAGGTACCTGCGGAACCTGGAGTGGCTGTTCGACCAAGTCGAAGATGGACCTCT
43► A L L S M D A L D L T D K L V S F Y L E

241 CCTACGGCGCCGAGCTCACCGCTAACGTGCTGCGCGACATGGGCCTGCAGGAGATGGCCG
GGATGCCCGCGGCTCGAGTGGCGATTGCACGACGCGCTGTACCCGGACGTCCTCTACCGGC
63► T Y G A E L T A N V L R D M G L Q E M A

301 GGCAGCTGCAGGCGGCCACGCACCAGGGCTCTGGAGCCGCGCCAGCTGGGATCCAGGCCC
CCGTCGACGTCCGCGCGGTGCGTGGTCCCGAGACCTCGGCGCGGTGACCCCTAGGTCCGGG
83► G Q L Q A A T H Q G S G A - A P A G I Q A

361 CTCCTCAGTCGGCAGCCCAAGCCAGGCCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA
GAGGAGTCAGCCGTCGGTTCGGTCCCGACGTGAAATATCTGGTTCGTGGCCCCGACGCGAAT
103► P P Q S A A K P G L H F I D Q H R A A L

421 TCGCGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCCTGACGG
AGCGCTCCCAAGTGTTCGCAACTACCGACGACCTACGAGACATGCCCTTCAGGACTGCC
123► I A R V T N V E W L L D A L Y G K V L T

481 ATGAGCAGTACCAGGCAGTGCAGGCGGAGCCACCAACCCAAGCAAGATGCGGAAGCTCT
TACTCGTCATGGTCCGTCACGCCCCGGCTCGGGTGGTTGGGTTCTACGCTTCGAGA
143► D E Q Y Q A V R A E P T N P S K M R K L

541 TCAGTTTCACACCAGCCTGGAAGTGGACCTGCAAGGACTTGCTCCTCCAGGCCCTAAGGG
AGTCAAAGTGTGGTCCGACCTTGACCTGGACGTTCTGAAACGAGGAGGTCCGGGATTCCC
163► F S F T P A W N W T C K D L L L Q A L R

601 AGTCCCAGTCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCAGCAACAC
TCAGGTCAGGATGGACCACCTCCTGGACCTCGCCTCGACTCCGAGGAAGGGTCGTTGTG
183► E S Q S Y L V E D L E R S

661 TCCGGTCAGCCCCCTGGCAATCCCAACCAATCATCCTGAATCTGATCTTTTTATACACAAT
AGGCCAGTCGGGGACCGTTAGGGTGGTTTAGTAGGACTTAGACTAGAAAAATATGTGTTA

721 ATACGAAAAGCCAGCTTGAA
TATGCTTTTCGGTCGAACTT

FIG. 21

ALIGN calculates a global alignment of two sequences

version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

> hCARD5-DNA 740 aa vs.

> mCARD5-DNA 763 aa

scoring matrix: paml20.mat, gap penalties: -12/-4

68.2% identity; Global alignment score: 2377

```

              10      20      30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC-----GGC
      :  ::::::::::::::: :::: :  .::: :::::::::::  :::
      CCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGGTGAC
              10      20      30      40      50      60

              40      50      60      70      80      90
inputs CGGGGAT-----CCTGGAGCCATGGGGCGCGCGCGCAGCCATCCTGGATGCGCTGGA
      :: :: :  :  ::::::::::::::: ::::: :  ::::::::::: :  :: ::
      CGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCACGAGATGCCATCCTGGACGCTCTTGA
              70      80      90      100     110     120

              100     110     120     130     140     150
inputs GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGTCGGTGCCGCTGCG
      .::: :::: :  :  ::::::::::::::: ::::::::::::::: ::::
      AAACCTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
              130     140     150     160     170     180

              160     170     180     190     200     210
inputs CGAGGGCTACGGGCGCATCCCCGCGGGGCGCGCTGCTGTCCATGGACGCTTGGACCTCAC
      ::::::::::: ::::::::::::::: :  :  :::::  ::::::::::::::: ::::
      AGAAGGCTATGGGCGCATCCCACGCGGGGCGCCTGCTGCAGATGGACGCCATAGATCTCAC
              190     200     210     220     230     240

              220     230     240     250     260     270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTCACCGCTAAC-GTGC
      ::::::::::: ::::::::::::::: ::::::::::: :  :  :  ::::::::::: .  :::: ::::
      TGACAAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
              250     260     270     280     290

              280     290     300     310     320     330
inputs TGC GCGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCAGGGCT
      :  :  ::::::::::: :::: :  :  ::::::::::::::: :  .  :  :  :  :  :  :
      TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGA--AGAG-T
      300     310     320     330     340     350

              340     350     360     370     380     390
inputs CTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAGCCAGGCCTGC
      ::::::::::: :  :  ::::: ..  :  :  :  :  :  :  :  :  :  :  :  :  :
      CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGG---AC
              360     370     380     390     400     410

              400     410     420     430     440     450

```

FIG. 23A


```

      690      700      710      720      730      740
inputs AAATCATCCTGAATCTGATCTTTTTATACACAATATACGAAAAGCCAGCTTGAA
      :::  .:  .:::.....: ::::.. .:::.. ::::.. :. ....
      AATTTTGA AAAACAATT-TGTATTGTGTTTAAAAAAAAAAAAAAAAAAGG
              720      730      740      750      760

```

FIG. 23B

ALIGN calculates a global alignment of two sequences

version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

> hCARD5-protein 195 aa vs.

> mCARD5-protein 193 aa

scoring matrix: pam120.mat, gap penalties: -12/-4

71.8% identity; Global alignment score: 712

```

      10      20      30      40      50      60
inputs MGRARDAILDALENLTAEELKKFKLKLLSVPLREGYGRIPRGALLSMDALDLTDKLVSFY
      .....
      MGRARDAILDALENLSGDELKKFKMKLLTVQLREGYGRIPRGALLQMDAIDLTDKLVSYY
      10      20      30      40      50      60

      70      80      90      100     110     120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQSGAAPAGIQAPPQSAAKPGLHFIDQHRA
      .....
      LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ
      70      80      90      100     110

      130     140     150     160     170     180
inputs ALIARVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMRKLFSFTPAWNWTCKDLLLQA
      .....
      ALIARVTEVDGVLDALHGSQLTEGQYQAVRAETTSQDKMRKLFSFVPSWNLTCKDSLLQA
      120     130     140     150     160     170

      190
inputs LRESQSYLVEDLERS
      ...
      LKEIHPYLVMDLEQS
      180     190

```

FIG. 24

1 CCCGCGTCCGGA CTTCCTTCCAGTGT TTTGTTCTCTCTGCTCTCTCCAACAGAAGGTATTTTGG
GGGCGCAGGCCTGAAGGGAAGGTCACAAACAAGGAGAGACGAGAGAGGTTGTCTTCCATAAAAAAC

66 GCATGTTTTATCTTTTGCTAAGTAGGATTTCTGTCTTTCTTTGTTAACACAGATTTCTTTCTGTGC
CGTACAAAATAGAAACGATTTCCTTAAAGACAGAAAGAAACAATTGTGTCTAAAGAAAGACAGC

131 CAGAATGACCTGATCCATTTCTGTTTGTAGAAAGCCATGGCTTCAGAGGGTGCTTCCTCAGAA
GTCTTACTGGACTAGGTAAAGGACCAAAACATCTTTCCGTACCGAAGTCTCCACGAAGGAGTCTT
----- 1 M A S E G A S S E -----

196 ATCATAGAAAAACAGCGAACAAAGTTGCTCAGTGTCTTCCAACAAGATCCCGACTCTATCTTGA
TAGTATCTTTTTGTGCTTGTTCACAGGAGTACAGGAGGTTGTTCTAGGGCTGAGATAGAACCT
----- 10 I I E K Q R T K L L S V L Q Q D P D S I L D -----

261 CACGTTAACCTCTCGGAGACTGATTTCTGAGGAGGAGTATGAGACTCTAGAGGCAATTACAGATC
GTGCAATTGGAGAGCCTCTGACTAAAGACTCTCTCTCATACTCTGAGATCTCCGTTAATGTCTAG
----- 31 T L T S R R L I S E E E Y E T L E A I T D -----

326 CTCTGAAGAAAAGCCGGAAGCTGTTAATTTTGATCCAGAAGAAGGGAGAGGACAGCTGTTGTGTG
GAGACTTCTTTTCGGCCTTCGACAATTAAACTAGGTCTTCTTCCCTCTCTGTGCGACAACAACA
----- 53 P L K K S R K L L I L I Q K K G E D S C C C -----

391 TTCCTCAAGTGTCTGTCTAATGCCTTTCCACAGTCAGCTTCCACCTTGGGTTTAAAGCAGGAAGT
AAGGAGTTACAGACAGATTACCGAAAGGTGTGAGTCAAGGTGGAACCCAAATTTCTGCTCCTCA
----- 75 F L K C L S N A F P Q S A S T L G L K Q E V -----

456 TCCACGGCAGGGGACTGGAGAGGTTGTGAGGTGAGCAGGGGTTTGGAAGATCCCTTTTCTCTTG
AGGTGCGCTCCCTGACCTCTCCAACAGCTCCACTCGTCCCCAAACCTTCTAGGGAAAAGAGAAC
----- 96 P R Q G T G E V V E V S R G L E D P F S L -----

521 GGACCATAACCCAGAAATAGCAGAGCTCTCAGAAGAGAAAGAATGCCCGGTCTGGGAGCTCCG
CCTGGTATTGGGGTCTTTATCGTCTCGAGAGTCTTCTCTTTCTTACGGGCCAGACCCTCGAGGC
----- 118 G T I T P E I A E L S E E K E C P G L G A P -----

586 GAGTTCTTACCTGCAAGGAAAGCAGCCACAGGGAACCGGAAGTACCTTCTTGGGAGAATCAGGA
CTCAAGAAGTGGACGTTCTTTCTGTCGGTGTCCCTTGGCCTTCATGGAAGAACCCTCTTAGTCCT
----- 140 E F F T C K E S S H R E P E V P S W E N Q E -----

651 AGGGCGTGGTGACAGCAAGTCACCGCTCCGCGTTCAGTCAAAGGAGTTGAGTATGAAGTTCCAG
TCCCGCACCAAGTGTGCTTCAAGTGGCGAGGCGCAAGTCAGTTTCTCAACTCATACTTCAAGGTC
----- 161 G R G A Q Q V T A P R S V K G V E Y E V P -----

FIG. 25A

716 CAAGTATCTCCCTCTTAAGCGACGGGCAGAGATACGAGGAGCCAGATGATTGCTGTACTTAGAA
GTTTCATAGAGGGAGAATTTCGCTGCCCGTCTCTATGCTCCTCGGTCTACTAAGCGACATGAATCTT
183▶ A S I S L L S D G Q R Y E E P D D S L Y L E

781 GAAGGGGAAGGTGAAGAGTCTCTTGGGTACCCTGAAGATGTTTTGGAGGAAGGGGCCGGCGATGA
CTTCCCCCTTCCACTTCTCAGAGAACCCATGGGACTTCTACAAAACCTCCTTCCCCGGCCGCTACT
205▶ E G E G E E S L G Y P E D V L E E G A G D D

846 CCCACAGTGCTTTGTATATGATAGTGAGGAGGAATGCGAGTATGAGGAAAACATGGGCTCCTCCG
GGGTGTCACGAAACATATACTATCACTCCTCCTTACGCTCATACTCCTTTTGTACCCGAGGAGGC
226▶ P Q C F V Y D S E E E C E Y E E N M G S S

911 GTGAAGACAGTAGCTGCGACGACACTTCAGAGACCTGCGTTCCATTGGAAGGGGAGAAAAGCGCT
CACTTCTGTGTCATCGACGCTGCTGTGAAGTCTCTGGACGCAAGGTAACCTTCCCCCTCTTTTCGCGA
248▶ G E D S S C D D T S E T C V P L E G E K S A

976 GAAGAAAGAAAAAGAGTGTTCACACGTCCTGTCTGTTTGAACATGGATAGAAACAGAAAGCT
CTTCTTTCTTTTCTCACAAGTTGTGACGAGCAGGACAAACTTGTACCTATCTTTGTCTTTTCGA
270▶ E E R K R V F Q H V L S C L N M D R N R K L

1041 TCTCCCAGAGTTTCGTGAGGCAGTTTTCATAGACCGAGGATGTGAGTGGACACCCAAGACCCAG
AGAGGGTCTCAAGCACTCCGTCAAAAGGTATCTGGCTCCTACACTCACCTGTGGGTCTGCGGTC
291▶ L P E F V R Q F S I D R G C E W T P K T P

1106 GAGACTTAGCTTGGAATTTCTTGATGAAAGTTCAGGCTTTAGACTCGACAGCCAGAGATTCTATC
CTCTGAATCGAACCTTAAAGAACTACTTTCAAGTCCGAAATCTGAGCTGTGGTCTCTAAGATAG
313▶ G D L A W N F L M K V Q A L D S T A R D S I

1171 CTGAGGCCCGAGGTGGCGGGTGAAGAGAATGAAGAATTGCCGGCTGGAATAGAGAAGTTAGGCAT
GACTCCGGGCTCCACCGCCCACTTCTCTTACTTCTTAACGCCGACCTTATCTCTTCAATCCGTA
335▶ L R P E V A G E E N E E L P A G I E K L G I

1236 TGGAGACCCCCAAACCATCCATCCCCTGGATGTCCTCTGCGCCTGCATGCTTTGTGCAGACAGCT
ACCTCTGGGGGTTTGGTAGGTAGGGGACCTACAGGAGACGCGGACGTACGAAACACGTCTGTCTGA
356▶ G D P Q T I H P L D V L C A C M L C A D S

1301 CCTTGCAGCGTGAAGTCATGTCAAACATGTACCAATGCCAGTTTGCTCTTCCCCTGCTACTGCCA
GGAACGTCGCACTTCACTACAGTTTGTACATGGTTACGGTCAAACGAGAAGGGGACGATGACGGT
378▶ S L Q R E V M S N M Y Q C Q F A L P L L L P

1366 GATGCTGAGAACAAACAAAACCTCTTAATGGTAGGGGCCATGAAGGACTTAAAGCAGCCCTCAGC
CTACGACTCTTGTTGTTTGGAGAATTACCATCCCCGGTACTTCTGAATTTGTCGGGAGTCG
400▶ D A E N N K N L L M V G A M K D L K Q P S A

FIG. 25B

1431 ACAGTCCTCAGGAGGGCCCTCAGGGAAACAGACACATTTCTGGGTCTCACAAAGATGCCTGTCA
TGTCAGGAGTCTCCCGGGAGTCCCTTTGTCTGTGTAAAGACCCAGAGTGTTCCTACGGACAGT
... 421▶ Q S S G G P L R E T D T F L G L T K M P V ...

1496 TCTCTTTTGTGCGACTAGGACGCTGCAGCTTCTCCAAGTCCAGAATTGTTAACACACTGCTCAGC
AGAGAAAACACGCTGATCCTGCGACGTCGAAGAGGTTTCAGGTCTTAACAATTGTGTGACGAGTCG
... 443▶ I S F V R L G R C S F S K S R I V N T L L S ...

1561 TCCTCCCAGCAGAAACCATACCCGATTTTCCTCCATCAGGATCTGTCTGTCCCTGTGCTTCCTCG
AGGAGGGTCTGCTTTTGGTATGGGCTAAAAGGAGGTAGTCTTAGACAGACAGGGACACGAAGGAGC
... 465▶ S S Q Q K P Y P I F L H Q D L S V P V L P R ...

1626 GCAAATTTCTGACGGCCTGGTGGAAGTGACATGGTGCTTTCTGACAAGTTGCTGAAGGAAAGCC
CGTTTAAAGACTGCCGGACCACCTTCACTGTACCACGAAAGGACTGTTCAACGACTTCCTTTTCGG
... 486▶ Q I S D G L V E V T W C F P D K L L K E S ...

1691 CGCATGCTTTCCAGAAACCTGTTGCTGTGGCCAACCTTCGTGGAGATTTAGAAAGCTTTTGGATA
GCGTACGAAAGGTCCTTTGGACAACGACACCGGTTGGAAGCACCTCTAAATCTTTTCGAAAACCTAT
... 508▶ P H A F Q K P V A V A N L R G D L E S F W I ...

1756 CAATTTGGTTTCTCGGTAGAAAGTTTCTCCGGTCTTTTCTTTTTCACAGACTGCCTTGGTGAGAA
GTTAAACCAAAGGACCATCTTCAAAGGAGGCCAGAAAAGAAAAAGTGTCTGACGGAACCACTCTT
... 530▶ Q F G F L V E V S S G L F F F T D C L G E K ...

1821 GGAATGGGACTTGCTAATGTTTTTAGGAGAGGACACCATTGAACGGTGCTACTTTATCCTCAGTC
CCTTACCCTGAACGATTACAAAAATCCTCTCCTGTGGTAACTTGCCACGATGAAATAGGAGTCAG
... 551▶ E W D L L M F L G E D T I E R C Y F I L S ...

1886 CCCAGGCTAAGGAGAGTGAAGAAGCCCAGATTTTCCAAGGATCCTAAAACCTGAAGCCATCTCAG
GGGTCCGATTCTCTCACTTCTTCGGGTCTAAAAGGTTTCTTAGGATTTTGAAGTTCGGTAGAGTC
... 573▶ P Q A K E S E E A Q I F Q R I L K L K P S Q ...

1951 CTACTGTTTTGGGAAGCTGAGGAAGCTGGGGATAGAAGGAAGACTATGGAGGCCCTTCAAGCTGC
GATGACAAAACCTTCGACTCCTTCGACCCCTATCTTCCTTCTGATACCTCCGGGAAGTTCGACG
... 595▶ L L F W E A E E A G D R R K T M E A L Q A A ...

2016 CCTCCAGGAAGTAATGTCCTCTCCACTCAGATGTGTGTCCCTTGAAGAGATGGCCTCTCTGGCCA
GGAGGTCTTTCATTACAGGAGAGGTGAGTCTACACACAGGGAACCTTCTTACCGGAGAGACCGGT
... 616▶ L Q E V M S S P L R C V S L E E M A S L A ...

2081 GGGAGCTGGGCATTTCAGGTAGACCAAGACTTTGAAGTTACTCAAGATATTCAAGTTTCCCCACA
CCCTCGACCCGTAAGTCCATCTGGTTCTGAAACTTCAATGAGTTCTATAAGTTCAAAGGGGGTGT
638▶ R E L G I Q V D Q D F E V T Q D I Q V S P T

FIG. 25C

2146 ACAGTTGAAGGTGAAAACCAACAACCATGTAGTCAGACCAAAGCCCGGCTGAAAGCGGAGCTCA
TGTCAACTTCCACTTTTGGTTGTTGGTACATCAGTCTGGTTTTCGGGCCGACTTTCGCCTCGAGT
... 660▶ T V E G E N Q Q P C S Q T K S P A E S G A Q ...

2211 GGAGCCAATCAGAGAGCCAGGGGCTCAATGTGACGACAGTCAGAATGCTCCGGTTTTCCATCAGA
CCTCGGTTAGTCTCTCGGTCCCCGAGTTACACTGCTGTGAGTCTTACGAGGCCAAAAGGTAGTCT
... 681▶ E P I R E P G A Q C D D S Q N A P V F H Q ...

2276 CTCCAGTATACATGCCTTATCCAGCACACCCATGGGCTTTGGCCATCAAAGCTGGAGGTAACTTT
GAGGTCAATATGTACGGAATAGGTCTGTGGGTACCCGAAACCGGTAGTTTCGACCTCCATTGAAA
... 703▶ T P V Y M P Y P A H P W A L A I K A G G N F ...

2341 TACCACGTTCCCTTTGAATGCCCCCTGGTTATGGGCTCCCACTTTGGATCACAGCAGAGGGCTAAG
ATGGTGCAAGGAACTTACGGGGGACCAATACCCGAGGGTGAAACCTAGTGTCTCTCCCGATTCT
... 725▶ Y H V P L N A P W L W A P T L D H S R G L S ...

2406 TGGTTCTTTCCATTCCCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAACTGCCACCATC
ACCAAGAAAGGTAAAGGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTGATTGACGGTGGTAG
... 746▶ G S F H S H A K P T H S K A F Q A N C H H ...

2471 CCCATCCCTCCCATGCTAAACCCACTCATGTGAATCCCTCTCATGCTAAACCCACTCATGTGCAG
GGGTAGGGAGGGTACGATTTGGGTGAGTACACTTAGGGAGAGTACGATTGGGGTGAGTACACGTC
... 768▶ P H P S H A K P T H V N P S H A N P T H V Q ...

2536 CCTTGCAATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAAACCCACTCCCTCTCAGACCTCT
GGAACGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTGATTGGGTGAGGGAGAGTCTGGAGA
... 790▶ P C M L N P L T L R P S K L N P L P L R P L ...

2601 TGGAGCCAAGCTAACTGCAATCATGCCATCCCTCCCTTGCTAAACCCCTCTCATACGAATCCCTC
ACCTCGGTTTCGATTGACGTTAGTACGGGTAGGGAGGGAACGATTTGGGAGAGTATGCTTAGGGAG
... 811▶ G A K L T A I M P I P P L L N P L I R I P ...

2666 TGATGCTAACCCCACTCATGTGCAGCCTTCCCATGCTAAACCCGCTCATCTACAGTCTTCCCAA
ACTACGATTGGGGTGAGTACACGTCGGAAGGGTACGATTTGGGCGAGTAGATGTCAGAAGGGTTT
... 833▶ L M L T P L M C S L P M L N P L I Y S L P K ...

2731 CAAAACCTCCCATCCCAATCTACTGCAGTTTCACGGCACACAAACCTCAGCAGTCCCAGTCTAA
GTTTTGGGAGGGGTAGGGTTAGATGACGTCAAGTGCCGTGTGTTTGGAGTCGTGAGGGTCAGATT
... 855▶ Q N P P H P N L L Q F T A H K P Q Q S Q S K ...

2796 GCCTTCTCAGCAGAGACCCAGTCAGCCTAAATCATTCCAGACCAAGCCTTCACAGGCCAGGGCCT
CGGAAGAGTCGTCTCTGGGTGAGTCGATTTAGTAAGGTCTGGTTCGGAAGTGTCCGGTCCCGGA
876▶ P S Q Q R P S Q P K S F Q T K P S Q A R A

FIG. 25D

2861 GCCACCCAAGAGCAGGGAGACGTTAAAGAACATACTCTGGAGATCTGGGAAATAAAGTATGGGCT
CGGTGGGTTCCTCGTCCCTCTGCAATTTCTTGATGAGACCTCTAGACCCTTTATTTCAACCCGA
898▶ C H P R A G R R -----

2926 TTGCTTAAGTATTCTTTTTTCATATAGCAAGCTGAAGAAAAGTTTTAGTGAAAGACTGATAAAAGT
AACGAATTCATAAGAAAAGTATATCGTTCGACTTCTTTTCAAAATCACTTTCTGACTATTTTCA-----

2991 AGCAAAACCCAAAAAGGTATGCAAAGTCTTAAGTGCATAGCAAAGTATCCAAGTGTGGGAAATA
TCGTTTTGGGTTTTTTTCCATACGTTTCAGAATTCACGTATCGTTTCATAGGTTACACCCCTTTAT-----

3056 TGGAAGCAGTTAAAAGTAGAATCTGGCTGGGCATGGTGGCACACATCTACAGGGTTTTAGCATGGG
ACCTTCGTCAATTTTCATCTTAGACCGACCCGTACCACCGTGTGTAGATGTCCCAAATCGTACCC-----

3121 AGGGCTCTGTCTATCCCAACTCAGAGAAGCAGGCAGATCTCTGTGTGTTTGAGGCCAGTCTGGTCT
TCCCGAGACAGTAGGGTTGAGTCTCTTCGTCCGTCTAGAGACACACAACTCCGGTCAGACCAGA-----

3186 ACATAACAACGACACAAGCAAGTCCTACATCAGCCATACTACAAAATGAGACCCCATCTGGGGAC
TGTATTGTGTGCTGTGTTTCGTTTCAGGATGTAGTCGGTATGATGTTTTACTCTGGGGTAGACCCCTG-----

3251 AAAAGGGTTGGATCTAACATCAAACCAAGAAATCAGTCAAGTATTCCAGAAGGCATCATTAAAT
TTTTCCCAACCTAGATTGTAGTTGGTTTTCTTTAGTCAGTTCATAAGGTCTTCCTGTAGTAATTAA-----

3316 ACACTCAGTGGGTTACCACAACCAACCATACTCGACAACCTAACCCCTAAAGGAGCAAGAAGGA
TGTGAGTCACCCAATGGTGTGGTTTGGTATGAGCTGTTGATTGGGGGATTTCTCTGTTCTTCCT-----

3381 GTTGGGTGGGTGTTAGGCTGAACATGATTGGGGAAGAACTGAAGATAGATAAGGTCAATTCGTAAT
CAACCCACCCACAATCCGACTTGTAATAACCCCTTCTTGACTTCTATCTATTCCAGTAAGCATTA-----

3446 ACAGGTTATGGGACTTGTCAAATCCATTAAATGCAATATTAAGAAGCAGTGGGAATCTTAAGGCT
TGTCCAATACCCCTGAACAGTTTAGGTAATTTACGTTATAATTCCTTCGTACCCCTTAGAATTCCTGA-----

3511 ACATTAAGCTCCAGTGAGTCGCAACCCCTCCCCTATTAGATGATGTGAGATTTGAACCCCACTGAA
TGTAATTCGAGGTCACCTCAGCGTTGGGAGGGGATAATCTACTACACTCTAAACTTGGGGTCACCT-----

3576 TGGGGTGTGTCTGATAGCCCGTGTGTGTGACAACTGTGTAATTATAAAGTGATGAAAACGTGGG
ACCCACACAGACTATCGGGCACACACTGTTTGACACATTAATATTTCACTACTTTTGCACCC-----

3641 AGTTCAGCTTATCTGTGTTGAAGAAAGGCTGCTTCAGAGGTGCCTTGGTTTTGGGTTTATGATCA
TCAAGTCAATAGACACAACCTTCTTTCCGACGAAGTCTCCACGGAACCAAAACCAATACTAGT-----

FIG. 25E

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3706 GCCACTGAGCAGATACTCTGCACCATTGGTACAGTTAAATCAGCTTGCTTCTGGTAATAGCCCCA
CGGTGACTCGTCTATGAGACGTGGTAACCATGTCAATTTAGTCGAACGAGACCATTATCGGGGT

3771 ATCTACCACATTTATCCCTTACAGGCGGAAATAATGAATGATCAGCAAAACATCCAATTTTACCT
TAGATGGTGTAAATAGGGAATGTCCGCCTTTATTACTTACTAGTCGTTTTGTAGGTTAAATGGA

3836 TAACCTTGGTACTGATTTGTATATGTATCATTCTTTATATAATAGCTAAGAAAAATTTAGCTCATT
ATTGGAACCATGACTAAACATATACATAGTAAGAAATATATTATCGATTCTTTTAAATCGAGTAA

3901 AGGGGTCTGATATATTAGTTTAAATGGTTTGAAGTCAGAAATGTGTTAGTTTAAATTTTAGAGT
TCCCAAGACTATATAATCAAATTTACCAAACTTCAGTCTTTACACAATCAAAATTTAAATCTCA

3966 TAATTGAAATATTGAGATGAATTTACAAAGGCTATAAGTAATGTTTGAGAGGGTTATAATTTTT
ATTAACTTTTATAACTCTACTTAAATGTTTCCGATATTCAATTACAACTCTCCCAATATTAAAA

4031 GTAGACTCATACTGTTCTGAACATTTGGATAGCTTCTCGTAGTTAGCAGTGTATAGAAGAATAT
CATCTGAGTATGACAAGACTTGTAAACCTATCGAAGAGCATCAATCGTCACAAATCTTCTTATA

4096 ATTTGATTTCAGGTATTTAACCAGAGCTGCTCTTAGTTTTTAAGTGTACCAAGAGTCAATAAAAG
TAAACTAAGTCCATAAATTGGTCTCGACGAGAATCAAAATTCACAGTGGTTCTCAGTTATTTTC

4161 GCTACATTATCTGAACATGTGGGAACACAACCTGTGACCTTACACTTAAGAGACTGAGGAAGGGAA
CGATGTAATAGACTTGTACACCCTTGTGTTGACACTGGAATGTGAATTCTCTGACTCCTTCCCTT

4226 ATCAAGGTTCAAGCCAGCAGCACATAGTGAGACCAGGTCTCAAGACACAAAACTATCCACCTTA
TAGTTCCAAGTTCGGTCGTCGTGTATCACTCTGGTCCAGAGTTCGTGTTTTTGTAGGTGGAAT

4291 AGGAAGATTTTAAAAATTTGCCTCATTAAGAAATAAAGTAAGATTTATAAATTGGACTAAATGTCA
TCCTTCTAAAAATTTAAACGGAGTAATCTTTATTTTCAATTCATAATTTTAACTGATTTACAGT

4356 CATCTTTGAACTTATGACTGTTTAAATTTTTTGAAGTTTAAATTTTATTATTGTATGCGTGT
GTAGAACTTGAATACTGACAAATTAATAAACTGAATTTCAAATTTAAATAATAACATACGCACA

4421 GTTGTATGTGTGTGCACATGTGTGCCACTGCATGTATGTGGAGGCCATCAGACAATGTTGTAGAG
CAACATACACACCGTGTACACACGGTGACGTACATACACCTCCGGTAGTCTGTTACAACATCTC

4486 TCTGTTCTTTCTCTTAGCCCTATGTGTTTTACCCACTGAGCTAGGCCACCTACTCCTATAAGTC
AGACAAGAAAGGAGAATCGGGATACAAAAATGGGTGACTCGATCCGGTGGATGAGGATATTTCAG

FIG. 25F

4551 TAATTTTAAATAGTAAATAGTTCTAAGAAGTCAATCAGGGAAAAAATGGCTGTCAAAGTCTCA
ATTAAATTTATCATTTTATCAAGATTCTTCAGTTAGTCCCTTTTTTTACCGACAGTTTCAGAGT

4616 AAGAAAAATCGTATTAGCCATGGATAGAGACTCACCTCTTGAATCATTGTGTCTGAGAATAGCC
TTCTTTTATAGCATAATCGGTACCTATCTCTGAGTGGAGAACTTAGTAAACACAGACTCTTATCGG

4681 TAATATCACAATAATGTGTTTGTACATGTGTTAGTTAATATTGTTTTTCAGAGTATTTAATCTCTC
ATTATAGTGTATTATACACAAACATGTACACAATCAATTATAACAAAAGTCTCATAAATTAGAGAG

4746 ATGATTATTGTAAAGATGAAAAAGAAATAGTGGGCAATGTATGTGAGTATTTAATTTTGCCTGA
TACTAATAACATTTCTACTTTTTTCTTTATCACCCGTTACATACACTCATAAATTAAACGGACT

4811 CAATTCTGTCTTTTAGAATGATAAATGTAAGAAGTAAAAATAAACGGTTTCATTCTCAGAACAACT
GTTAAGACAGAAAATCTTACTATTTACATTCTTCATTTTATTTTGCCAAGTAAGAGTCTTGTGTA

4876 AAGCCAGCTCACTTAAGTCTGGGCCCTGCTGGCATTGGCTAGTCTAGCTACCCCCACCCAAACAC
TTCGGTCGAGTGAATTCAGACCCGGGACGACCGTAACCGATCAGATCGATGGGGGTGGGTTTGTG

4941 AAAAGTTTAGAGAAGAAAATGACTGAGTCAAGCTTGCCTAATGACTTTTGGACATAAAGTTTATG
TTTTCAAATCTCTTCTTTTACTGACTCAGTTCTGAACGGATTACTGAAAACCTGTATTTCAAATAC

5006 GTCCTAGAAAGCCTTAAAATAAGTAGGATATAAAACATGTAAATTAACCCACACATTATGTGGGT
CAGGATCTTTTCGGAATTTTATTCATCCTATATTTTGTACATTTAATTGGGTGTGTAATACACCCA

5071 TGAGAAGCAGAAAAATGTCAGTAGAACACTCGGCCAGTGCATAAAGAAGGAAGAGACCTCTGTTT
ACTCTTCGTCTTTTACAGTCATCTTGTGAGCCGGTCACGTATTTCTTCTTCTCTGGAGACAAG

5136 TGGGTTATAAACTGCTCTTTGTGCTCAATTTGTCCCCTGCTTTTGTGTTGCCAGAATGTACAAGA
ACCCAATATTTTGACGAGAAACACGAGTTAAACAGGGGACGAAAACAAACGGTCTTACATGTTCT

5201 TTATAAAATAAACTCACTTTTACTTTTAAAAAATAAAAAAAAAAAGGGCGG
AATATTTTATTTGAGTGAAAATGAAAATTTTTTTTTTTTTTTTTTTTTCCTCCGCC

FIG. 25G

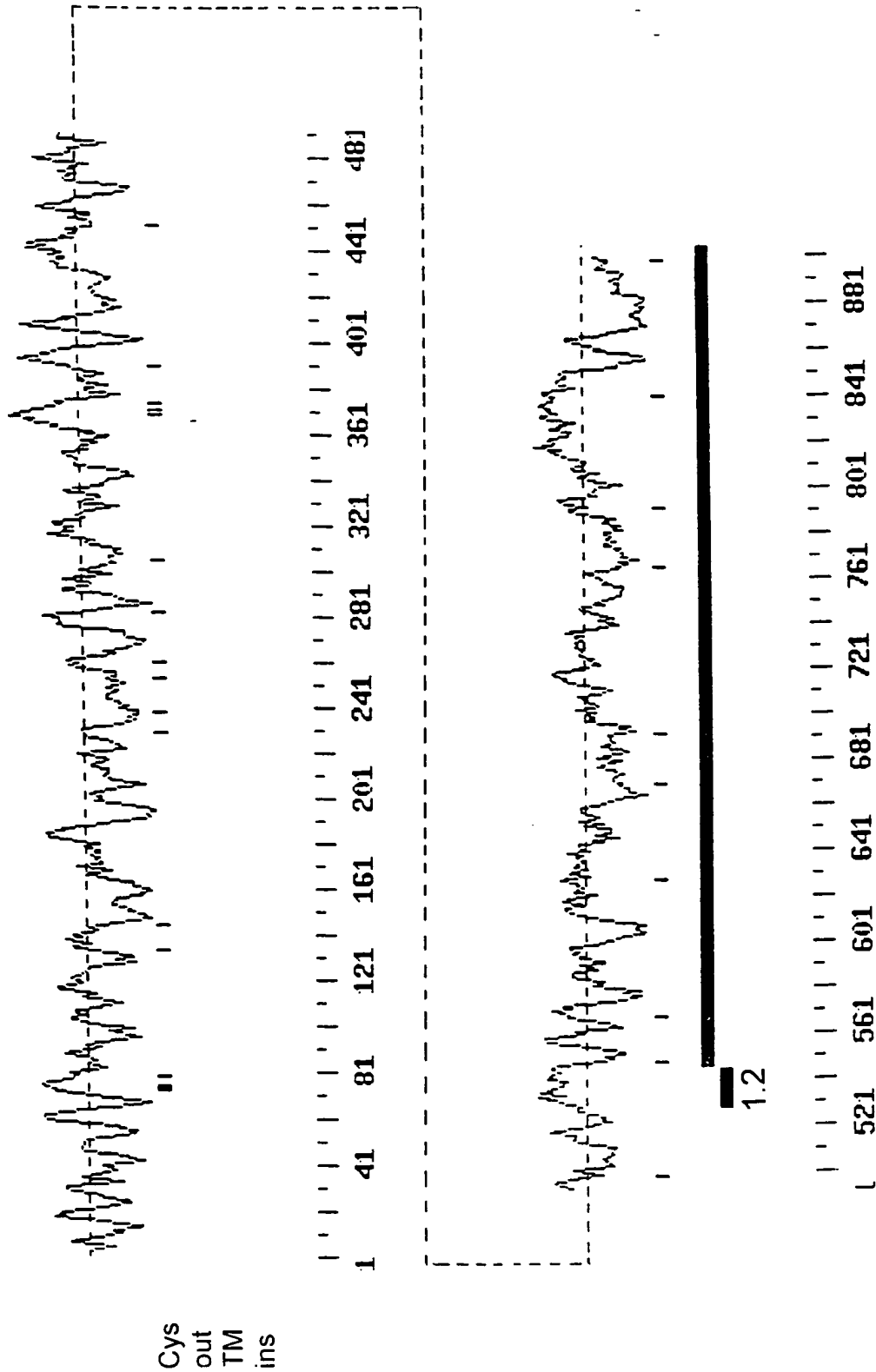
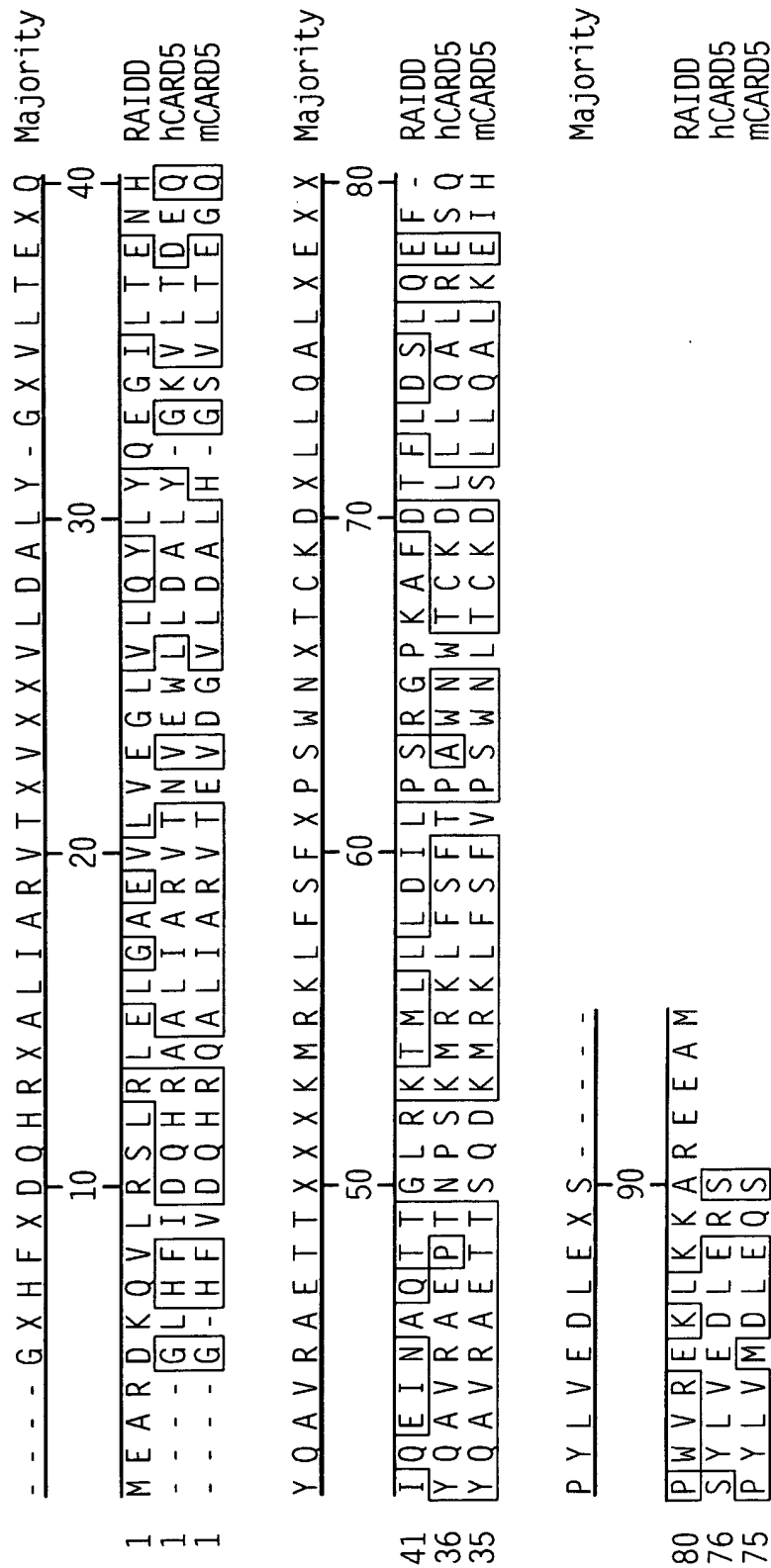


FIG. 26



CACGCGTCCGCCGGATCAGAGAGTGCTCCGAGCTGGGTTGCCCCACTGTGCTTGATCTGCACTCTCCAACACTAGGC 79
ATCATTGACATGTTAAAGCTTAGCCAAATAGAATTGTTCTTTGTGCTTCTTTTTTAACTTTTACTTATTCATTAGGAT 158
M A T E S T P S E 9
GATTTTCATAATATATTTCTCGGTTTAGAGGAAACAGGAACA ATG GCT ACC GAG AGT ACT CCC TCA GAG 226
I I E R E R K K L L E I L Q H D P D S I 29
ATC ATA GAA AGA GAA AGA AAA AAG TTG CTT GAA ATC CTT CAA CAT GAT CCT GAT TCT ATC 286
L D T L T S R R L I S E E E Y E T L E N 49
TTA GAC ACG TTA ACT TCT CGG AGG CTG ATT TCT GAG GAA GAG TAT GAG ACT CTG GAG AAT 346
V T D L L K K S R K L L I L V Q K K G E 69
GTT ACA GAT CTC CTG AAG AAA AGT CGG AAG CTG TTA ATT TTG GTA CAG AAA AAG GGA GAG 406
A T C Q H F L K C L F S T F P Q L A A I 89
GCG ACC TGT CAG CAT TTT CTC AAG TGT TTA TTT AGT ACT TTT CCA CAG TTA GCT GCC ATT 466
C G L R H E V L K H E N T V P P Q S M G 109
TGC GGC TTA AGG CAT GAA GTT TTA AAA CAT GAG AAT ACA GTA CCT CCT CAA TCT ATG GGG 526
A S S N S E D A F S P G I K Q P E A P E 129
GCA AGC AGT AAT TCA GAA GAT GCT TTT TCT CCT GGA ATA AAA CAG CCT GAA GCC CCT GAG 586
I T V F F S E K E H L D L E T S E F F R 149
ATC ACA GTG TTC TTC AGT GAG AAG GAA CAC TTG GAT TTG GAA ACC TCT GAG TTT TTC AGG 646
D K K T S Y R E T A L S A R K N E K E Y 169
GAC AAG AAA ACT AGT TAT AGG GAA ACA GCT TTG TCT GCC AGG AAG AAT GAG AAG GAA TAT 706
D T P E V T L S Y S V E K V G C E V P A 189
GAC ACA CCA GAA GTC ACA TTA TCA TAT TCA GTT GAG AAA GTT GGA TGT GAA GTT CCA GCA 766
T I T Y I K D G Q R Y E E L D D S L Y L 209
ACT ATT ACA TAT ATA AAA GAT GGA CAG AGA TAT GAG GAG CTA GAT GAT TCT TTA TAC TTA 826
G K E E Y L G S V D T P E D A E A T V E 229
GGA AAA GAG GAA TAT CTA GGA TCT GTT GAC ACC CCT GAA GAT GCA GAA GCC ACT GTG GAA 886
E E V Y D D P E H V G Y D G E E D F E N 249
GAG GAG GTT TAT GAT GAC CCA GAG CAC GTT GGA TAT GAT GGT GAA GAG GAC TTC GAG AAT 946
S E T T E F S G E E P S Y E G S E T S L 269
TCA GAA ACC ACA GAG TTC TCT GGT GAA GAA CCA AGT TAT GAG GGA TCA GAA ACC AGC CTT 1006
S L E E E Q E K S I E E R K K V F K D V 289
TCA TTG GAG GAG GAA CAG GAG AAA AGT ATA GAA GAA AGA AAA AAG GTG TTT AAA GAT GTC 1066
L L C L N M D R S R K V L P D F V K Q F 309
CTG TTA TGT TTG AAC ATG GAT AGA AGC AGA AAG GTT CTG CCA GAT TTT GTT AAA CAA TTC 1126
S L D R G C K W T P E S P G D L A W N F 329
TCC TTA GAT CGA GGA TGT AAG TGG ACC CCT GAG AGT CCA GGA GAC TTA GCC TGG AAT TTC 1186
L M K V Q A R D V T A R D S I L S H K V 349
CTG ATG AAA GTT CAA GCA CGA GAT GTG ACG GCT AGG GAT TCA ATC CTC AGT CAC AAG GTT 1246
L D E D S K E D L L A G V E N L E I R D 369
CTG GAT GAA GAT AGC AAG GAG GAT TTG CTG GCT GGA GTG GAG AAT TTG GAA ATT CGA GAC 1306

FIG. 28A

I Q T I N P L D V L C A T M L C S D S S 389
ATA CAA ACC ATT AAT CCC CTT GAC GTG CTT TGT GCC ACC ATG CTG TGT TCA GAT AGC TCT 1366

L Q R Q V M S N M Y Q C Q F A L P L L L 409
TTG CAA CGC CAA GTC ATG TCA AAC ATG TAT CAG TGC CAG TTT GCT CTT CCC CTG CTA CTG 1426

P D A E N N K S I L M L G A M K D I V K 429
CCA GAT GCA GAA AAC AAC AAA AGC ATC TTA ATG CTG GGG GCC ATG AAA GAC ATT GTG AAG 1486

K Q S T Q F S G G P T E D T E K F L T L 449
AAG CAG TCA ACA CAG TTT TCA GGG GGG CCT ACA GAG GAT ACA GAA AAG TTT CTG ACT CTC 1546

M K M P V I S F V R L G Y C S F S K S R 469
ATG AAG ATG CCT GTC ATC TCT TTT GTG CGT CTA GGA TAC TGT AGC TTC TCT AAG TCC AGA 1606

I L N T L L S P A Q L K L H K I F L H Q 489
ATC CTC AAC ACA CTT CTC AGC CCT GCC CAG TTG AAA TTA CAC AAA ATC TTT CTT CAT CAA 1666

D L P L L V L P R Q I S D G L V E I T W 509
GAT TTG CCT CTT TTG GTG CTT CCC CGG CAA ATC TCT GAT GGC CTG GTT GAG ATA ACA TGG 1726

C F P D S D D R K E N P F F Q K P V A L 529
TGT TTT CCT GAT AGC GAT GAT AGA AAG GAA AAC CCC TTT TTC CAA AAG CCT GTT GCT CTG 1786

A N L R G N L E S F W T Q F G F L M E V 549
GCT AAT CTC CGT GGA AAT CTA GAA AGT TTT TGG ACT CAG TTT GGT TTT TTG ATG GAA GTT 1846

S S A V F F F T D C L G E K E W D L L M 569
TCT TCA GCT GTG TTT TTT TTC ACT GAC TGT TTA GGT GAG AAG GAA TGG GAC TTG CTA ATG 1906

F L G E A A I E R C Y F V L S S Q A R E 589
TTT TTA GGA GAG GCT GCC ATT GAA AGA TGC TAC TTT GTT CTC AGT TCC CAA GCC AGG GAG 1966

S E E A Q I F Q R I L N L K P A Q L L F 609
AGT GAA GAG GCT CAA ATT TTT CAG AGG ATA CTG AAC TTG AAG CCA GCA CAG CTA CTG TTT 2026

W E R G D A G D R R K N M E G L Q A A L 629
TGG GAG AGG GGA GAT GCT GGG GAT AGA AGG AAG AAC ATG GAG GGC CTT CAA GCT GCC CTC 2086

Q E V M F S S C L R C V S V E D M A A L 649
CAG GAA GTG ATG TTC TCT TCT TGC CTC AGA TGT GTG TCT GTG GAG GAT ATG GCC GCC CTG 2146

A R E L G I Q V D E D F E N T Q R I Q V 669
GCC AGG GAG CTG GGG ATT CAG GTA GAT GAA GAC TTT GAA AAC ACT CAG AGA ATT CAA GTT 2206

S S G E N M A G T A E G E G Q Q R H S Q 689
TCC TCT GGA GAA AAC ATG GCT GGG ACA GCT GAA GGT GAG GGT CAG CAA AGA CAC AGT CAG 2266

L K S S S K S Q A L M P I Q E P G T Q C 709
CTA AAA AGC TCA TCT AAA AGC CAG GCT CTA ATG CCA ATT CAA GAG CCT GGG ACT CAA TGT 2326

E L S Q N L Q N L Y G T P V F R P V L E 729
GAG CTC AGC CAG AAT CTT CAG AAT CTC TAT GGT ACC CCA GTA TTC AGG CCT GTT CTA GAG 2386

N S W L F P T R I G G N F N H V S L K A 749
AAC TCC TGG CTC TTT CCA ACC AGA ATT GGA GGT AAC TTT AAC CAT GTT TCC TTG AAA GCC 2446

S W V M G R P F G S E Q R P K W F H P L 769
TCC TGG GTT ATG GGC CGC CCC TTT GGG TCA GAG CAG AGG CCT AAG TGG TTC CAT CCT TTG 2506

FIG. 28B

P F Q N A G A Q G R G K S F G I Q S F H 789
CCT TTT CAG AAT GCA GGG GCC CAG GGC CGA GGT AAA AGT TTT GGT ATT CAA TCC TTC CAT 2566

P Q I F Y S G E R F M K F S R V A R G C 809
CCC CAG ATA TTT TAT TCA GGT GAA AGA TTC ATG AAA TTT TCC AGA GTT GCT CGG GGA TGT 2626

H S N G T F G R L P R P I C Q H V Q A C 829
CAC TCG AAT GGA ACA TTT GGG AGA CTG CCA AGA CCC ATT TGT CAG CAT GTA CAG GCC TGC 2686

P E R P Q M M G T L E R S R A V A S K I 849
CCT GAG AGA CCA CAA ATG ATG GGA ACT CTT GAA AGG TCT AGG GCA GTA GCC TCC AAG ATA 2746

G H S Y S L D S Q P A R A V G K P W P Q 869
GGT CAC TCC TAT TCC CTG GAT TCA CAG CCA GCA AGA GCA GTA GGG AAG CCA TGG CCT CAG 2806

Q A C T R V T E L T E A T G K L I R T S 889
CAA GCT TGC ACC AGG GTA ACA GAG TTA ACT GAA GCA ACT GGA AAA CTG ATA AGA ACA TCC 2866

H I G K P H P Q S F Q P A A A T Q K L R 909
CAT ATT GGA AAG CCT CAC CCT CAG TCC TTT CAA CCA GCA GCA GCC ACA CAA AAA CTA AGA 2926

P A S Q Q G V Q M K T Q G G A S N P A L 929
CCT GCT TCT CAG CAA GGA GTC CAG ATG AAG ACA CAA GGT GGG GCT TCA AAT CCA GCT CTC 2986

Q I G S H P M C K S S Q F K S D Q S N P 949
CAA ATA GGG TCC CAT CCC ATG TGC AAG AGC TCT CAG TTC AAA TCC GAT CAG TCC AAC CCA 3046

S T V K H S Q P K P F H S V P S Q P K S 969
TCC ACA GTC AAA CAC TCC CAG CCT AAA CCC TTC CAT TCT GTG CCC TCT CAA CCT AAA TCC 3106

S Q T K S C Q S Q P S Q T K P S P C K S 989
TCT CAG ACA AAA TCC TGT CAG TCC CAG CCC TCC CAA ACT AAA CCT TCT CCA TGC AAA TCT 3166

T Q P K P S Q P W P P Q S K P S Q P R P 1009
ACT CAG CCT AAG CCA AGC CAG CCC TGG CCT CCC CAG TCT AAG CCT TCT CAG CCC AGA CCC 3226

P Q P K S S S T N P S Q A K A H H S K A 1029
CCT CAA CCT AAG TCA TCC TCA ACC AAT CCT TCA CAA GCT AAG GCA CAC CAC TCA AAA GCA 3286

G Q K R G G K H * 1038
GGG CAG AAG AGG GGA GGG AAG CAT TAA 3313

AGAGCTAACTCCAGAGATCTATAAAGCATATCCTTTACCCAGGCCATTCTATCATATAGTAAGCAGAAGAGTTGCCAT 3392

GAAAGTAAAGACTACTGTCTATTAGCATGTAAAACAAAGAAAGATATACATGACCGAATTGGATATCTTTGTTTGTGTTG 3471

TTTGAGACAGAGTTTCACTCTTGTTGCCAGGCTGGAGTGCAATGGCAGCATCTCGGCTCACCGCAACCTCTGCTTCCT 3550

GGCTTAAAGTGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCACCACCACACCCAGCTAATTTTG 3629

TATTTTATAGTAGAGGCAGGGTTTCTCCATGTTGGTCAAGCTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCCACCTA 3708

GGCCTCTCAAAGTGTTGGGATTACGTGTGTAAGCCACAGTGCCCGACCCGAATTGGATATCTTTAAGATATCTGTAAGT 3787

GTTATATCCCTAACCAAGAAGAAAAATATGAAAATAATTAAGACTAGAAATCAAGCAGTAGATAATTGAATCCAATCTTG 3866

GGTATTATTAGATAATGTATAACTTGCACCCAGGGAATGGGGGTCTATGAGACAACCCCACTTGGAGAAGAATGGGGTT 3945

AGGGTCTCTAATTGCAAAGTGACTGTACAATAGGACGAAAGTTGCCTCTGTGTCTGAGAAAGTATCTTAGTTGTTGGCT 4024

FIG. 28C

GCTCCAGAGGTATCTTTGTCAAAAAGCTTCTGGTTCAATATCAGCCACTGAGCAGATAACCTGCTTATTTGGTGTGGTT 4103
AAATCCACTAGCTTCTGCTAATAGCCCCCAATTTGCTTGAATGGGAAAACCTCTCTCATTGACCCCTTATAGGTAGAAAATA 4182
ATGAATTAAACAACCAATAAAATTATCATTTTGGCATTAAAAAAAATAAAAAAARAAA 4244

FIG. 28D

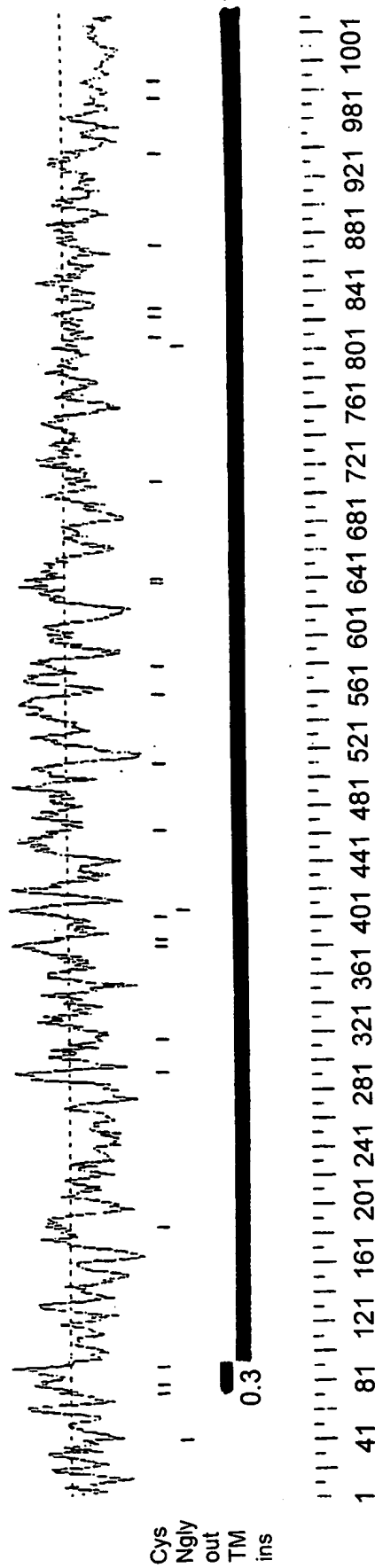


FIG. 29


```
CONSENSUS      *->maederrlLkknrvrliesLgldvLdelldvLlekdvlnlkeeEkik
                +++ + ++ r++l+e+L+ d +Ld L +++++ ++e E
CARD6          5   STP--SEIIERERKKLLEILQHD-PDSILDTLTSRRLISEEYETLE 48

CONSENSUS      ragakledDKarelvdsLqrrgsqafdaIdaledTggsyLAdvLel<-*
                + 1 + r l++ +q++g. + ++ f+ +l++ LA++ +l
CARD6          49 NVTDLLKK--SRKLLILVQKKGEATCQHFLKCLFS-TFPQLAAICGL 92
```

FIG. 30

	- A - E S - G S E I I D Q H R X A L L A R V T E D P - D S L L D A L L S R D L I	Majority
	10 20 30 40	
1	I A Q Q W - - - - I I Q S K R E D I V N Q M I E A C L N Q S L D A L L S R D L I	hCARD3-CARD
1	- - - E S H P H I Q L L K S N R E L L V T H I R N T - Q C L V D N L L K N D Y F	hCARD4-CARD
1	- - - - - G L H F I D Q H R A A L I A R V T N - - V E W L L D A L L Y G K - V L	hCARD5-CARD
1	- - - - - G - H F V D Q H R Q A L I A R V T E - - V D G V L D A L L H G S - V L	mCARD5-CARD
1	M A S T E S T P S E I I E R E R K K L L E I L Q H D P - D S I L D T L T S R R L I	hCARD6-CARD
1	M A S E G A S S E I I E K Q R T K L L S V L Q Q D P - D S I L D T L T S R R L I	rCARD6-CARD
	S E E D Y E A V E A E T T X L S K V R K L L I L V Q S K G E E T C K - F L K C L	Majority
	50 60 70 80	
36	M K E D Y E L V S T K P T T R T S K V R Q L L D T T D I Q G E E - - - - F A F V I	hCARD3-CARD
37	S A E D A F I V C A C P T T Q P D K K V R K I L D L V Q S K G E E V S E F F L - Y L	hCARD4-CARD
32	T D E Q Y Q A V R A E P T N P S K M R K K L F S F T P A W - N W T C K - - - D L L	hCARD5-CARD
31	T E G Q Y Q A V R A E T T S Q D K K M R K K L F S F V P S W - N L T C K - - - D S L	mCARD5-CARD
40	S E E E Y E T L E A I T T D L L E N V T T D L K K S R K L L I L V Q K G E A T C Q H F L K C L	hCARD6-CARD
40	S E E E Y E T L E A I T T D L L E N V T T D L K K S R K L L I L V Q K G E D S C C F L K C L	rCARD6-CARD
	L O A L K D S A A Y L G L D P E V - - - - - L E - S	Majority
	90 100	
72	V Q K L K D N K Q - M G L Q P Y P - - - - - F I L	hCARD3-CARD
76	L Q Q L A D I - - A Y V D L R P W L	hCARD4-CARD
68	L Q A L R E S Q S Y L V E D - - - - - L E R S	hCARD5-CARD
67	L Q A L K E I H P Y L V M D - - - - - L E Q S	mCARD5-CARD
80	F S T F P Q L A A I C G L R H E V L	hCARD6-CARD
80	S N A F P Q S A S T L G L K Q E V P R Q G T G E V V F V S	rCARD6-CARD

FIG. 31